







## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LCM2469 row: f column: 10  
 High quality sequence start: 5  
 High quality sequence stop: 696.  
 Location/Qualifiers  
 1. .992  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6279561"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_113"  
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCAAGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

## FEATURES

source

## ORIGIN

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Query Match      83.6%; Score 265.8; DB 13; Length 992;
Best Local Similarity 89.9%; Pred. No. 1.4e-69;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy  2  AGCTACCCAGTCTCCATGCTCTGCTGCTCTGTAGGAGACAGAGTCACCATCACTT 61
Db  105 AGATGACCCAGTCTCCATGCTCTGCTGCTCTGTAGGAGACAGAGTCACCATCACTT 164

Qy  62  GCCGGGACGTCAGAGTATTAGACCTATTAAATTGGTATCAGCAGAAACCGGGGAAG 121
Db  165 GCCGGGCAAGTCAGAGTATTAGACCTTTTAAATTGGTATCAGCAGAAACCGGAAAG 224

Qy  122 CCCCTAAGCTCCTGATCTGTAGTCATCCCAATTTGCAAGTGGGTCCCATCCAGGTCA 181
Db  225 CCCCTACTCTCGTGAUCTTTGCTGCATCCAAATTTGCAAGTGGGTCCCATCAAGGTCA 284

Qy  182 GTGGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGACT 241
Db  285 GTGGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCCGTCTGCAACCTGAAGATT 344

Qy  242 TTGCAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACCA 301
Db  345 TTGCAGTTACTACTGTCAACAGAGTTACATACCCCTGGACGTTCCGGCCAAGGGACCA 404

Qy  302 AACTGGAGATCAAAACGA 318
Db  405 AGGTGGGAATCAAAACGA 421

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Search completed: August 13, 2004, 07:13:24  
 Job time : 1865.96 secs

mis Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 207.182 Seconds  
(without alignments)  
6520.490 Million cell updates/sec

Title: US-10-027-725A-5  
Perfect score: 318  
Sequence: 1 gagctaccacgtctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316.4	99.5	318	6	ABK89641 DNA encod
2	276.4	86.9	321	5	Aah68647 Human ant
3	276.4	86.9	321	5	Aah68701 Human ant
4	276.4	86.9	321	8	ACD45311 Anti-Rh(D
5	276.4	86.9	321	8	ACD45365 Anti-Rh(D
6	273.4	86.0	315	2	AAV19761 Antibody
7	273.2	85.9	321	5	Aah68720 Human ant
8	273.2	85.9	321	5	Aah68658 Human ant
9	273.2	85.9	321	5	Aah68652 Human ant
10	273.2	85.9	321	5	Aah68713 Human ant
11	273.2	85.9	321	5	Aah68703 Human ant
12	273.2	85.9	321	8	ACD45377 Anti-Rh(D
13	273.2	85.9	321	8	ACD45367 Anti-Rh(D
14	273.2	85.9	321	8	ACD45384 Anti-Rh(D
15	273.2	85.9	321	8	ACD45316 Anti-Rh(D
16	273.2	85.9	321	8	ACD45322 Anti-Rh(D
17	271.6	85.4	321	5	Aah68723 Human ant
18	271.6	85.4	321	5	Aah68651 Human ant
19	271.6	85.4	321	5	Aah68724 Human ant
20	271.6	85.4	321	5	Aah68707 Human ant
21	271.6	85.4	321	8	ACD45371 Anti-Rh(D
22	271.6	85.4	321	8	ACD45388 Anti-Rh(D
23	271.6	85.4	321	8	ACD45387 Anti-Rh(D

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24 271.6 85.4 321 8 ACD45315
25 271.2 85.3 720 2 AAX36070
26 271.2 85.3 720 7 ABZ76706
27 270.6 85.1 396 2 AAT75423
28 270 84.9 321 5 AAH68717
29 270 84.9 321 5 AAH68719
30 270 84.9 321 8 ACD45383
31 270 84.9 321 8 ACD45381
32 269 84.6 729 3 AAA11630
33 269 84.6 729 6 ABL46009
34 268.4 84.4 321 5 AAH68650
35 268.4 84.4 321 8 ACD45314
36 268.4 84.4 321 4 AAH47727
37 268 84.3 324 7 AAL52122
38 268 84.3 324 7 AAL52120
39 268 84.3 333 5 AAH74684
40 268 84.3 333 7 ABT34320
41 268 84.3 900 5 AAH74688
42 268 84.3 900 7 ABT34324
43 267.4 84.1 324 4 AAF29073
44 267.4 84.1 333 5 AAH74685
45 267.4 84.1 333 7 ABT34321

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## ALIGNMENTS

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RESULT 1
ABK89641
ID ABK89641 standard; DNA; 318 BP.
XX
AC ABK89641;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 60 light chain.
XX
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
PH
CDS
FT
FT /*tag= a
FT /product= "Fab clone 60 heavy chain"
FT /transl_except= (pos:292..294, aa:Ser)
FT misc_feature 7..63
FT /*tag= b
FT /note= "FR1 region"
FT misc_feature 64..96
FT /*tag= c
FT /note= "CDR1 region"
FT misc_feature 97..141
FT /*tag= d
FT /note= "FR2 region"
FT misc_feature 142..162
FT /*tag= e
FT /note= "CDR2 region"
FT misc_feature 163..258
FT /*tag= f
FT /note= "FR3 region"
FT misc_feature 259..285
FT /*tag= g
FT /note= "CDR3 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
PR

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XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
PA Flicker S, Steinberger P, Kraft D, Valenta R;  
XX P-PSDB; ABG30449.  
XX WPI; 2002-583604/62.  
DR P-PSDB; ABG30449.  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX Disclosure; Page 35; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi p 2. The present sequence represents the DNA  
CC encoding the human IgG fab, clone 60 light chain protein of the invention  
XX  
XX Sequence 318 BP; 83 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

Query Match 99.5%; Score 316.4; DB 6; Length 318;  
Best Local Similarity 99.7%; Pred. No. 9.7e-92;  
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAGCTCACCCAGTCTCCATCTCCCTCTGCTGCTCTGCTAGGACAGAGTCCACCATCACT 60  
DB 1 GAGCTCACCCAGTCTCCATCTCCCTCTGCTGCTCTGCTAGGACAGAGTCCACCATCACT 60  
QY 61 TGCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGACAGAAACCGGGGAAG 120  
DB 61 TGCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGACAGAAACCGGGGAAG 120  
QY 121 GCCCTTAAGCTCCTGATCTGAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
DB 121 GCCCTTAAGCTCCTGATCTGAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
QY 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATATACCTTCGGCCCTGGGACC 300  
DB 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATATACCTTCGGCCCTGGGACC 300  
QY 301 AAACCTGGAGATCAACAGA 318  
DB 301 AAACCTGGAGATCAACAGA 318

RESULT 2  
AAH68647  
ID AAH68647 standard; DNA; 321 BP.  
XX AAH68647;  
AC  
XX  
XX 14-SEP-2001 (first entry)  
XX Human anti-Rh(D) chain 102 nucleotide sequence.  
DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
XX  
KW

red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
XX Homo sapiens.  
XX US6255455-B1.  
XX 03-JUL-2001.  
XX 29-JAN-1999; 99US-00240274.  
XX 11-OCT-1996; 96US-0028550P.  
XX 27-JUN-1997; 97US-00884045.  
XX 10-APR-1998; 98US-0081380P.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX Siegel DL;  
XX WPI; 2001-388931/41.  
XX P-PSDB; AAG93590.  
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.  
XX Example 2; Col 54; 162pp; English.  
XX The present invention describes an isolated Rh(D) binding protein,  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93598 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
CC are used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention  
XX  
XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;  
Query Match 86.9%; Score 276.4; DB 5; Length 321;  
Best Local Similarity 91.8%; Pred. No. 7.7e-79;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 1 GAGCTCACCCAGTCTCCATCTCCCTCTGCTGCTCTGCTAGGACAGAGTCCACCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTCTGCTGCTCTGCTAGGACAGAGTCCACCATCACT 63  
QY 61 TGCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGACAGAAACCGGGGAAG 120  
DB 64 TGCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGACAGAAACCGGGGAAG 123  
QY 121 GCCCTTAAGCTCCTGATCTGAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTTCGCAAGTGGGTCCCATCCAGGTTTC 183  
QY 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 184 AGTGCAGTGGATCTGGACAGAGTTCATCTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATATACCTTCGGCCCTGGGACC 300  
DB 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATATACCTTCGGCCCTGGGACC 303  
QY 301 AAACCTGGAGATCAACAGA 318  
DB 304 AAGGTGGAATCAACAGA 321  
RESULT 3  
AAH68701  
ID AAH68701 standard; DNA; 321 BP.

XX AAH68701;  
 AC 14-SEP-2001 (first entry)  
 DT Human anti-Rh(D) antibody clone SH13 nucleotide sequence.  
 XX  
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6255455-B1.  
 XX 03-JUL-2001.  
 PD 29-JAN-1999; 99US-00240274.  
 XX  
 XX 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Siegel DL;  
 XX  
 PI WPI; 2001-388931/41.  
 XX P-PSDB; AAG93644.  
 DR  
 DR New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 XX diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 PT  
 XX Example 3; Col 74; 162pp; English.  
 PS  
 XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;  
 Query Match 86.9%; Score 276.4; DB 5; Length 321;  
 Best Local Similarity 91.8%; Pred. No. 7.7e-79;  
 Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 QY 1 GAGTCACCCAGTCTCCATCTCCTCTGTGCTCTGTAGGACAGAGTCACCATCACT 60  
 DB 4 GAGTCACCCAGTCTCCATCTCCTCTGTGCTCTGTAGGACAGAGTCACCATCACT 63  
 QY 61 TGCGGGCAGTCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGGAAG 120  
 DB 64 TGCGGGCAGTCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGGAAG 123  
 QY 121 GCCCCTAAGTCTCTGATCTGTAGTCATCCAAATTGCAAGTGGGTCCCATCCAGGTT 180  
 DB 124 GCCCCTAAGTCTCTGATCTGTAGTCATCCAAATTGCAAGTGGGTCCCATCCAGGTT 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACCTGAAGAC 240  
 DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACCTGAAGAT 243  
 QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATACCTTGGGCCCTGGGACC 300  
 DB 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATACCTTGGGCCCTGGGACC 303

QY 301 AACTGGAGTCAACGA 318  
 DB 304 AAGCTGGAGTCAACGA 321  
 RESULT 4  
 ACD45311  
 ID ACD45311 standard; DNA; 321 BP.  
 XX  
 AC ACD45311;  
 XX  
 DT 12-SEP-2003 (first entry)  
 XX  
 DE Anti-Rh(D) chain I02 DNA.  
 XX  
 KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;  
 KW magnetically activated cell sorting.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003040605-A1.  
 XX 27-FEB-2003.  
 PD  
 XX 04-MAY-2001; 2001US-00848798.  
 XX  
 XX 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 XX  
 XX WPI; 2003-512273/48.  
 DR P-PSDB; ABO27397.  
 DR  
 XX New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 PT  
 XX Claim 12; Page 39; 187pp; English.  
 PS  
 XX The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents DNA encoding a human anti-Rh(D) chain  
 XX  
 SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;  
 Query Match 86.9%; Score 276.4; DB 8; Length 321;  
 Best Local Similarity 91.8%; Pred. No. 7.7e-79;  
 Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 QY 1 GAGTCACCCAGTCTCCATCTCCTCTGTGCTCTGTAGGACAGAGTCACCATCACT 60  
 DB 4 GAGTCACCCAGTCTCCATCTCCTCTGTGCTCTGTAGGACAGAGTCACCATCACT 63  
 QY 61 TGCGGGCAGTCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGGAAG 120  
 DB 64 TGCGGGCAGTCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGGAAG 123  
 QY 121 GCCCCTAAGTCTCTGATCTGTAGTCATCCAAATTGCAAGTGGGTCCCATCCAGGTT 180  
 DB 124 GCCCCTAAGTCTCTGATCTGTAGTCATCCAAATTGCAAGTGGGTCCCATCCAGGTT 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACCTGAAGAC 240  
 DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACCTGAAGAT 243  
 QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATACCTTGGGCCCTGGGACC 300



Db 61 TCGCGGCAAGTCAGACATTAGACGCTATTAAATTGGTATCAGCAGAAACCGGAAA 120  
 QY 121 GCCCCTAAGCTCTCTGATCTGTAGTCGATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTT 180  
 Db 121 GCCCCTAAGCTCTCTGATCTGTAGTCGATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTT 180  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCATCTGCAACCTGAAGAC 240  
 Db 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCATCTGCAACCTGAAGAT 240  
 QY 241 TTGCAAGTCTACTACTGCAACAGAGTTACACTACCTTATATATACCTTCGGGCCCTGGGACC 300  
 Db 241 TTGCAACTTACTACTGCAACAGAGTTTCACTCTCACCATCAGCATCTGCAACCTGAAGAT 240  
 QY 301 AAAGTGGATATCAAA 315  
 Db 301 AAAGTGGATATCAAA 315

RESULT 7  
 AAH68720  
 ID AAH68720 standard; DNA; 321 BP.  
 XX AC AAH68720;  
 XX AC AAH68720;  
 DT 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) antibody clone SH49 nucleotide sequence.  
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
 XX Homo sapiens.  
 OS US6255455-B1.  
 PN 03-JUL-2001.  
 PD 29-JAN-1999; 99US-00240274.  
 XX 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 PI WPI; 2001-388931/41.  
 DR P-PSDB; AAG93663.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX Example 3; Col 79; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;  
 Query Match 85.9%; Score 273.2; DB 5; Length 321;

Best Local Similarity 91.2%; Pred. No. 8.3e-78;  
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 GAGTCACCCAGCTCCATCTCCCTGCTCTGTCCTCTGTAGGAGACAGAGTCACCATCACT 60  
 Db 4 GAGTCACCCAGCTCCATCTCCCTGCTCTGTCCTCTGTAGGAGACAGAGTCACCATCACT 63  
 QY 61 TGGCGGCGAGTCAGAGTATTAGACCTATTAAATTGGTATCAGCAGAAACCGGGAAG 120  
 Db 64 TGGCGGCGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCGGGAAG 123  
 QY 121 GCCCCTAAGCTCTCTGATCTGTAGTCGATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTT 180  
 Db 124 GCCCCTAAGCTCTCTGATCTGTAGTCGATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTT 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCATCTGCAACCTGAAGAC 240  
 Db 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCATCTGCAACCTGAAGAT 243  
 QY 241 TTGCAAGTCTACTACTGCAACAGAGTTACACTACCTTATATATACCTTCGGGCCCTGGGACC 300  
 Db 244 TTGCAACTTACTACTGCAACAGAGTTTCACTCTCACCATCAGCATCTGCAACCTGAAGAT 243  
 QY 301 AAAGTGGATATCAAA 318  
 Db 304 AAGTGGAAATCAACGA 321

RESULT 8  
 AAH68658  
 ID AAH68658 standard; DNA; 321 BP.  
 XX AC AAH68658;  
 XX AC AAH68658;  
 DT 14-SEP-2001 (first entry)  
 XX Human anti-Rh(D) chain I13 nucleotide sequence.  
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.  
 XX Homo sapiens.  
 OS US6255455-B1.  
 PN 03-JUL-2001.  
 PD 29-JAN-1999; 99US-00240274.  
 XX 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Siegel DL;  
 PI WPI; 2001-388931/41.  
 DR P-PSDB; AAG93601.  
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX Example 2; Col 57; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC the present invention  
 XX SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;  
 Query Match 85.9%; Score 273.2; DB 5; Length 321;





```
DR WPI; 2001-388931/41.
DR P-PSDB; AAG93656.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX
PS Example 3; Col 77; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 8.3e-78;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGTCAACCCAGTCTCCATCTCCCTGTCTGCTCTCTAGGAGACAGAGTCACCATCACT 60
Dd |||||
Dd 4 GAGTCAACCCAGTCTCCATCTCCCTGTCTGCTCTCTAGGAGACAGAGTCACCATCACT 63
QY 121 GCCCTAAGCTCTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 180
Dd |||||
Dd 124 TCCCTAAGCTCTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCCATCAGCAATCTGCAACCTGAAGAC 240
Dd |||||
Dd 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCCATCAGCAATCTGCAACCTGAAGAT 243
QY 241 TTTCGAAGTTTACTGTCTCAACAGAGTTTACACTACCTTATATATACCTTCGGCCCTGGGACC 300
Dd |||||
Dd 244 TTTCGAAGTTTACTGTCTCAACAGAGTTTACACTACCTTATATATACCTTCGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACCGA 318
Dd |||||
Dd 304 AAAGTGGAGATCAACCGA 321
RESULT 11
AAH68703
ID AAH68703 standard; DNA; 321 BP.
XX
AC AAH68703;
XX
DT 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH16 nucleotide sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX Homo sapiens.
XX
XX OS
XX US6255455-B1.
XX
XX PN
XX 03-JUL-2001.
XX
XX PD
XX 29-JAN-1999; 99US-00240274.
XX
XX
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PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
XX P-PSDB; AAG93646.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
XX
XX Example 3; Col 75; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
SQ Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 8.3e-78;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGTCAACCCAGTCTCCATCTCCCTGTCTGCTCTCTAGGAGACAGAGTCACCATCACT 60
Dd |||||
Dd 4 GAGTCAACCCAGTCTCCATCTCCCTGTCTGCTCTCTAGGAGACAGAGTCACCATCACT 63
QY 61 TGGCGGCAGTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 120
Dd |||||
Dd 64 TGGCGGCAGTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 123
QY 121 GCCCTAAGCTCTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 180
Dd |||||
Dd 124 GCCCTAAGCTCTCTGATCTAGTGCATCCAAATTTGCAAGTGGGGTCCCATCAGGTTT 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCCATCAGCAATCTGCAACCTGAAGAC 240
Dd |||||
Dd 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCCATCAGCAATCTGCAACCTGAAGAT 243
QY 241 TTTCGAAGTTTACTGTCTCAACAGAGTTTACACTACCTTATATATACCTTCGGCCCTGGGACC 300
Dd |||||
Dd 244 TTTCGAAGTTTACTGTCTCAACAGAGTTTACACTACCTTATATATACCTTCGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACCGA 318
Dd |||||
Dd 304 AAAGTGGAGATCAACCGA 321
RESULT 12
ACD45377
ID ACD45377 standard; DNA; 321 BP.
XX
XX ACD45377;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) light chain SH36 DNA.
XX
XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
XX magnetically activated cell sorting.
XX
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OS Homo sapiens.  
 PN US2003040605-A1.  
 PD 27-FEB-2003.  
 PF 04-MAY-2001; 2001US-00848798.  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Siegel DL;  
 PI WPI; 2003-512273/48.  
 DR P-PSDB; ABO27463.  
 XX New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.  
 PT Claim 12; Page 60; 187pp; English.  
 XX The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain  
 SQ Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;  
 Query Match 85.9%; Score 273.2; DB 8; Length 321;  
 Best Local Similarity 91.2%; Pred. No. 8.3e-78;  
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 GAGCTCACCCAGTCTCCATCCTCCCTGCTGCTGTAGGAGACAGAGTCACCATCACT 60  
 DB 4 GAGCTCACTCAGTCTCCATCCTCCCTGCTGCTGTAGGAGACAGAGTCACCATCACT 63  
 QY 61 TCCCGGGCAGTCGAGATTTAGACCTATTTAAATTTGGTATCAGAGAAACCGGGGAAG 120  
 DB 64 TCCCGGGCAGTCAGAGATTTAGCAGCTATTTAAATTTGGTATCAGAGAAACCGGGGA 123  
 QY 121 GCCCTTAAGCTCCTGATCTGATGTCATCCAAATTTGCAAAGTGGGTCCTCCAGGTTTC 180  
 DB 124 TCCCTTAAGCTCCTGATCTGATGTCATCCAAATTTGCAAAGTGGGTCCTCCAGGTTTC 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC 240  
 DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAT 243  
 QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGCCCTGGGACC 300  
 DB 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGCCCTGGGACC 303  
 QY 301 AAACCTGGAGATCAACGA 318  
 DB 304 AAAGTGGATATCAACGA 321

RESULT 13  
 ACD45367  
 ID ACD45367 standard; DNA; 321 BP.  
 XX AC ACD45367;  
 XX 12-SEP-2003 (first entry)  
 XX Anti-Rh(D) light chain SH16 DNA.  
 XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;

KW magnetically activated cell sorting.  
 XX Homo sapiens.  
 PN US2003040605-A1.  
 PD 27-FEB-2003.  
 PF 04-MAY-2001; 2001US-00848798.  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 PA Siegel DL;  
 PI WPI; 2003-512273/48.  
 DR P-PSDB; ABO27453.  
 XX New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.  
 PT Claim 12; Page 57; 187pp; English.  
 XX The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain  
 SQ Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;  
 Query Match 85.9%; Score 273.2; DB 8; Length 321;  
 Best Local Similarity 91.2%; Pred. No. 8.3e-78;  
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 QY 1 GAGCTCACCCAGTCTCCATCCTCCCTGCTGCTGTAGGAGACAGAGTCACCATCACT 60  
 DB 4 GAGCTCACCCAGTCTCCATCCTCCCTGCTGCTGTAGGAGACAGAGTCACCATCACT 63  
 QY 61 TCCCGGGCAGTCGAGATTTAGCAGCTATTTAAATTTGGTATCAGAGAAACCGGGGAAG 120  
 DB 64 TCCCGGGCAGTCAGAGATTTAGCAGCTATTTAAATTTGGTATCAGAGAAACCGGGGA 123  
 QY 121 GCCCTTAAGCTCCTGATCTGATGTCATCCAAATTTGCAAAGTGGGTCCTCCAGGTTTC 180  
 DB 124 GCCCTTAAGCTCCTGATCTGATGTCATCCAAATTTGCAAAGTGGGTCCTCCAGGTTTC 183  
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC 240  
 DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAT 243  
 QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGGCCCTGGGACC 300  
 DB 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGGCCCTGGGACC 303  
 QY 301 AAACCTGGAGATCAACGA 318  
 DB 304 AAGTGGAGATCAACGA 321

RESULT 14  
 ACD45384  
 ID ACD45384 standard; DNA; 321 BP.  
 XX AC ACD45384;  
 XX 12-SEP-2003 (first entry)  
 XX Anti-Rh(D) light chain SH49 DNA.







Db 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTCAACCTTGAAGAC 240  
QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTGGCCCTGGGACC 300  
Db 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTGGCCCTGGGACC 300  
QY 301 AAACCTGGAGATCAACGA 318  
Db 301 AAACCTGGAGATCAACGA 318

RESULT 2  
US-09-848-798-102  
; Sequence 102, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain I02  
US-09-848-798-102

Query Match 86.9%; Score 276.4; DB 10; Length 321;  
Best Local Similarity 91.8%; Pred. No. 2e-85;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 1 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGCTAGGACAGAGTCAACATCACT 60  
Db 4 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGCTAGGACAGAGTCAACATCACT 63  
QY 61 TCCCGGGCAGCTCAGAGTATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAA 120  
Db 64 TCCCGGGCAGCTCAGAGTATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAA 123  
QY 121 GCCCTTAAGCTCCTGATCTGTAGTGCATCCAAATTTGCAAGTGGGCTCCATCCAGGTTTC 180  
Db 124 GCCCTTAAGCTCCTGATCTGTAGTGCATCCAGTTTGGCAAGTGGGCTCCATCCAGGTTTC 183  
QY 181 AGTGCAGTGTGATCTGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGCAGTGTGATCTGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTGGCCCTGGGACC 300  
Db 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTGGCCCTGGGACC 303  
QY 301 AAACCTGGAGATCAACGA 318  
Db 304 AAGGTGGAAATCAACGA 321

RESULT 3  
US-09-848-798-199  
; Sequence 199, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 199  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-09-848-798-199

Query Match 86.9%; Score 276.4; DB 10; Length 321;  
Best Local Similarity 91.8%; Pred. No. 2e-85;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 1 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGCTAGGACAGAGTCAACATCACT 60  
Db 4 GAGCTCACCCAGTCTCCATCTCCCTGTCTGCTGCTAGGACAGAGTCAACATCACT 63  
QY 61 TCCCGGGCAGCTCAGAGTATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAA 120  
Db 64 TCCCGGGCAGCTCAGAGTATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAA 123  
QY 121 GCCCTTAAGCTCCTGATCTGTAGTGCATCCAAATTTGCAAGTGGGCTCCATCCAGGTTTC 180  
Db 124 GCCCTTAAGCTCCTGATCTGTAGTGCATCCAGTTTGGCAAGTGGGCTCCATCCAGGTTTC 183  
QY 181 AGTGCAGTGTGATCTGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGCAGTGTGATCTGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
QY 241 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACC 300  
Db 244 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACC 303  
QY 301 AAACCTGGAGATCAACGA 318  
Db 304 AAGCTGGAGATCAACGA 321

RESULT 4  
US-09-848-798-107  
; Sequence 107, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain I07  
US-09-848-798-107

Query Match 85.9%; Score 273.2; DB 10; Length 321;



Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 60  
Db |||||  
Qy 4 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 63  
Db |||||  
Qy 61 TGCGGGCAGCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAAAACCGGGGAG 120  
Db |||||  
Qy 64 TGCGGGCAAGTCAGAGCAITAGCAGCTATTAAATTGGTATCAGCAAAACCGGGGAA 123  
Db |||||  
Qy 121 GCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCCAGGTT 180  
Db |||||  
Qy 124 GCCCTAAGCTCTCTGATCTGTGCTATCCAGTTGCAAGTGGGGTCCCATCAAGGTT 183  
Db |||||  
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACTGAAGAC 240  
Db |||||  
Qy 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243  
Db |||||  
Qy 241 TTGCAAGTTACTACTCTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
Db |||||  
Qy 244 TTGCAACTTACTACTCTCAACAGAGTTACAGTACCTCCCTGCACTTTTCGGCGGGGAGC 303  
Db |||||  
Qy 301 AAAGTGGAGATCAAAACA 318  
Db |||||  
Qy 304 AAGTGGAGATCAAAACA 321  
Db |||||

## RESULT 5

US-09-848-798-113  
; Sequence 113, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 113  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 113  
US-09-848-798-113

Query Match 85.9%; Score 273.2; DB 10; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 60  
Db |||||  
Qy 4 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 63  
Db |||||  
Qy 61 TGCGGGCAGCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAAAACCGGGGAG 120  
Db |||||  
Qy 64 TGCGGGCAAGTCAGAGCAITAGCAGGTAITAAATTGGTATCAGCAAAACCGGGGAA 123  
Db |||||  
Qy 121 GCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCCAGGTT 180  
Db |||||  
Qy 124 GCCCTAAGCTCTCTGATCTGTGCTATCCAGTTGCAAGTGGGGTCCCATCAAGGTT 183  
Db |||||  
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTACCATCAGCAATCTGCAACTGAAGAC 240  
Db |||||  
Qy 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243  
Db |||||

Qy 241 TTGCAAGTTACTACTCTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
Db |||||  
Qy 244 TTGCAACTTACTACTCTCAACAGAGTTACGTTACCGTACCCCTCAGTCTTTGCGCGGGGAGC 303  
Db |||||  
Qy 301 AAAGTGGAGATCAAAACA 318  
Db |||||  
Qy 304 AAGTGGAGATCAAAACA 321  
Db |||||

## RESULT 6

US-09-848-798-201  
; Sequence 201, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 201  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16  
US-09-848-798-201

Query Match 85.9%; Score 273.2; DB 10; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 60  
Db |||||  
Qy 4 GAGTCAACCCAGTCTCCATCTCCCTGTGCTCTGTAGGACAGAGTCACCATCACT 63  
Db |||||  
Qy 61 TGCGGGCAGCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAAAACCGGGGAG 120  
Db |||||  
Qy 64 TGCGGGCAAGTCAGAGCAITAGCAGCTATTAAATTGGTATCAGCAAAACCGGGGAA 123  
Db |||||  
Qy 121 GCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCCAGGTT 180  
Db |||||  
Qy 124 GCCCTAAGCTCTCTGATCTGTGCTATCCAGTTGCAAAAGTGGGGTCCCATCAAGGTT 183  
Db |||||  
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCAACTGAAGAC 240  
Db |||||  
Qy 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243  
Db |||||  
Qy 241 TTGCAAGTTACTACTCTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
Db |||||  
Qy 244 TTGCAACTTACTACTCTCAACAGAGTTACAGTACCTCCCTCAGTCTTTGCGGGGAGC 303  
Db |||||  
Qy 301 AAAGTGGAGATCAAAACA 318  
Db |||||  
Qy 304 AAGTGGAGATCAAAACA 321  
Db |||||

## RESULT 7

US-09-848-798-211  
; Sequence 211, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798

; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 211  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36  
US-09-848-798-211

Query Match 85.9%; Score 273.2; DB 10; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
  
QY 1 GAGCTCACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 63  
  
QY 61 TCCCGGCGACGTCAGAGATTAGCACCTATTAAATTTGGTATCAGCAGAAACCGGGGAAG 120  
DB 64 TCCCGGCGAAGTCAGAGCATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAAA 123  
  
QY 121 GCCCTTAAGCTCCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTTC 180  
DB 124 TCCCTTAAGCTCCTGATCTATGCTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTTTC 183  
  
QY 181 AGTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTCAACCTCAAGAC 240  
DB 184 AGTGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTCAAGAT 243  
  
QY 241 TTTGCAAGTTACTACTGTCAACAGAGTTTACACTTATATACCTTCGGCCCTGGGACC 300  
DB 244 TTTGCAACTTACTACTGTCAACAGAGTTTACAGTACCCCGTGGACGTTTCGGCCCTGGGACC 303  
  
QY 301 AAACCTGGAGATCAACGA 318  
DB 304 AAAGTGGATATCAACGA 321

RESULT 8  
US-09-848-798-218  
; Sequence 218, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 218  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-848-798-218

Query Match 85.9%; Score 273.2; DB 10; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GAGCTCACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 63  
  
QY 61 TCCCGGCGACGTCAGAGATTAGCACCTATTAAATTTGGTATCAGCAGAAACCGGGGAAG 120  
DB 64 TCCCGGCGAAGTCAGAGCATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAAA 123  
  
QY 121 GCCCTTAAGCTCCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTTC 180  
DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTTTC 183  
  
QY 181 AGTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTCAACCTCAAGAC 240  
DB 184 AGTGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTCAAGAT 243  
  
QY 241 TTTGCAAGTTACTACTGTCAACAGAGTTTACACTTATATACCTTCGGCCCTGGGACC 300  
DB 244 TTTGCAACTTACTACTGTCAACAGAGTTTACAGTACCCCGTGGACGTTTCGGCCCAAGGACC 303  
  
QY 301 AAACCTGGAGATCAACGA 318  
DB 304 AAAGTGGATATCAACGA 321

RESULT 9  
US-10-309-762-115  
; Sequence 115, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; FILE REFERENCE: ABGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 384  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-309-762-115

Query Match 85.6%; Score 272.2; DB 16; Length 384;  
Best Local Similarity 91.2%; Pred. No. 6.3e-84;  
Matches 289; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
  
QY 2 AGCTCACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 61  
DB 68 AGATGACCCAGTCTCCATCCTCCTGCTGCTAGGAGACAGAGTCAACATCACT 127  
  
QY 62 GCCCGGCGACGTCAGAGATTAGCACCTATTAAATTTGGTATCAGCAGAAACCGGGGAAG 121  
DB 128 GCCCGGCGAAGTCAGAGCATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCGGGGAAA 187  
  
QY 122 CCCCTTAAGCTCCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGGTTTC 181  
DB 188 CCCCTTAAGCTCCTGATCTATGCTGATCCATCCATTTGCGAGTGGGGTCCCATCAAGTTTC 247  
  
QY 182 GTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTCAAGACT 241  
DB 248 GTGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCGGTTCTGCAACCTCAAGATT 307  
  
QY 242 TTGCAAGTTACTACTGTCAACAGAGTTTACACTTATATACCTTCGGCCCTGGGACC 301  
DB 308 TTGCAACTTACTACTGTCAACAGAGTTTACAGTTCCTTATTCATTTTCGGCCCTGGGACC 367

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Qy      302 AACTGGAGATCAACGA 318
        |||||
Db      368 AAGTGGATCAACGA 384

RESULT 10
US-09-848-798-106
; Sequence 106, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIORITY FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: arti-Rh(D) chain I06
US-09-848-798-106

```

Query Match	85.4%	Score	271.6	DB	10	Length	321
Best Local Similarity	90.9%	Pred. No.	9.5e-84				
Matches	289	Conservative	0	Mismatches	29	Indels	0
Gaps	0						
Qy	1	GAGCTCACCCAGTCTCCATCTCCCTGCTCTGCCTCTGTAGGAGACAGAGTCACCATCACT	60				
Db	4	GAGCTCACCCAGTCTCCATCTCCCTGCTCTGCATCTGTAGGAGACAGAGTCACCATCACT	63				
Qy	61	TGCCGGGCAGCTCAGAGTATTAGCACCTATTTTAAATTGGTATCAGCAGAAACCGGGGAAG	120				
Db	64	TGCCGGGCAGTCAAGCATTTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGGAAA	123				
Qy	121	GCCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGGTCCCATCCAGGTTTC	180				
Db	124	GCCCCTTAAGCTCTGATCTATGCGGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC	183				
Qy	181	AGTGGCAGTGGATCTGGCAGAGTTTCATCTCTACCATCAGCATCTGCRACCTTGAGAC	240				
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTCTACCATCAGCAGTCTGCAACCTTGAAGAT	243				
Qy	241	TTTGTCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGGCCCTGGGACC	300				
Db	244	TTTGTCACTTACTGTGTCAACAGAGTTACAGTACCCCGATCACTTCGGCCCAAGGGACA	303				
Qy	301	AAACTGGAGATCAAAACGA	318				
Db	304	CGACTGGAGATTAACGA	321				

RESULT 11  
US-09-848-798-205  
; Sequence 205, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550

```

; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 205
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-09-848-798-205

Query Match      85.4%; Score 271.6; DB 10; Length 321;
Best Local Similarity 90.9%; Pred. No. 9.5e-84;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 GAGCTCACCCAGTCTCCATCCTCCCTCTCTGCGCTCTCTAGGAGACAGAGTCACCATCACT 60
Db 4 GAGCTCACCCAGTCTCCATCCTCCCTCTCTGCGATCTCTAGGAGACAGAGTCACCATCACT 63
Qy 61 TGGCGGCACGCTCAGAGTATTAGCACCTATTAAATTTGGTATCAGCAGAAACCGGGGAAG 120
Db 64 TGGCGGCACGCTCAGACATTAGCACCTATTAAATTTGGTATCAGCAGACACCGAGGAAA 123
Qy 121 GCCCTAAGCTCCTGATCTCTAGTGCATCAAAATTTGCAAAAGTGGGGTCCCATCCAGGTTTC 180
Db 124 GCCCTAACCTCCTGATCTATGTCATCCACITTTGCAAAAGGGGGTCCCATCAAGGTTTC 183
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240
Db 184 ACTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCATCTCTGCAACCTGAAGAT 243
Qy 241 TTTGCAAGTTTACTACTGTCTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300
Db 244 TTTGCAACTTTACTACTGTCTCAACAGAGTTACACTACCTGTGGAGCTTCGGCCCAAGGGACC 303
Qy 301 AAACCTGGAGATCAAAACGA 318
Db 304 AAGATGGAATCAGACGA 321

RESULT 12
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

```

	Query Match	85.4%	Score 271.6	DB 10	Length 321
	Best Local Similarity	90.9%	Pred. No. 9.5e-84		
	Matches 289	Conservative	0	Mismatches 29	Indels 0
	Gaps	0			
Qy	1	GAGTCAACCCAGTCTCCATCCTCCCTGTGCGCTCTGTAGGACACAGATCACCATCACT	60		
Db	4	GAGTCAACCCAGTCTCCATCCTCCATGTCTGCACTCTGTAGGACACAGATCACCATCACT	63		

Qy	61	TGCCGGGCGACTCAGAGTATTAGCACTATTATAATTTGGTATCAGCAGAAACCGGGGAA	120
Db	64	TGCCGGGCAAGTCAGAGCATTTGGCACTTATTATAATTTGGTATCAGCAGAAACCGGGAAA	123
Qy	121	GCCCTTAAGCTCCTGATCTGTAGTGCATCCAAATTTGAAAGTGGGTCCCATCCAGGTTC	180
Db	124	GCCCTTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAGGTTC	183
Qy	181	AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGTCAACCTGAAGAT	243
Qy	241	TTTGCAAGTTACTACTGTCAACAGAGTTACACTCTTATATACCTTGGCCCTCGGACC	300
Db	244	TTTGCAACTTACTACTGTCAACAGAGTTACAGTCCCGTGGACGTTGGCCCAAGGACC	303
Qy	301	AAACTGGAGATCAACGA	318
Db	304	AAGGTGGAAATCAACGA	321

RESULT 13  
US-09-848-798-222  
; Sequence 222, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 222  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-222

RESULT 14  
US-09-192

```

US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION: Greg
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

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RESULT 15

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US-09-968-561A-1
? Sequence 1, Application US/09968561A
? Patent No. US20020164642A1
? GENERAL INFORMATION:
? APPLICANT: Tomlinson, Ian M
? APPLICANT: Winter, Gregory
? TITLE OF INVENTION: Method to Screen Phage
? FILE REFERENCE: 8039/1073B
? CURRENT APPLICATION NUMBER: US/09/968,561A
? CURRENT FILING DATE: 2001-10-01
? PRIOR APPLICATION NUMBER: GB 9722131.1
? PRIOR FILING DATE: 1997-10-20
? PRIOR APPLICATION NUMBER: US 60/065,248
? PRIOR FILING DATE: 1997-11-13
? PRIOR APPLICATION NUMBER: US 60/066,729
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: PCT/GB98/03135
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: US 09/511,939
? PRIOR FILING DATE: 2000-02-24

```









Db 304 AAGTGGAAATCAAACGA 321

## RESULT 2

US-09-240-274-199  
; Sequence 199, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:

```

; APPLICANT: Siegel, Donald L.
;
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;
; FILE REFERENCE: 09596-42U2
;
; CURRENT APPLICATION NUMBER: US/09/240,274
;
; CURRENT FILING DATE: 1999-01-29
;
; EARLIER APPLICATION NUMBER: 60/081,380
;
; EARLIER FILING DATE: 1998-04-10
;
; EARLIER APPLICATION NUMBER: 60/028,550
;
; EARLIER FILING DATE: 1996-10-11
;
; NUMBER OF SEQ ID NOS: 224
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 199
;
; LENGTH: 321

```

US-09-240-274-199

Query Match 86.9%; Score 276.4; DB 3; Length 321;  
Best Local Similarity 91.8%; Pred. No. 2e-85;  
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy	1	GAGCTCACCCAGTCTCCATCTCTCCCTGTCTGCTCTGTAGGAGACAGAGTCACCAATCACT	60
Db	4	GAGCTCACCCAGTCTCCATCTCTCCCTGTCTGCTCTGTAGGAGACAGAGTCACCAATCACT	63
Qy	61	TGCGGGGCAGCTTCAGAGTATTAGCACTTATTAAATTTGGTATCAGCAGAAAAACGGGGGAAG	120
Db	64	TGCGGGGCAAGTCAGAGCATTTAGCAGCTATTTTAAATTTGGTATCAGCAGAAAAACGGGAAA	123
Qy	121	GCCCGTAAGCTCCGTGATCTGTAGTCATCCAAATTTTGCAAGTGGGGTCCCATCCAGGTTTC	180
Db	124	GCCCGTAAGCTCCGTGATCTGTGTGCATCCAGTTTTCGCAAGTGGGGTCCCATCAAGGTTTC	183
Qy	181	AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAGCATCAGCAAACTGTGCAACTCGAAGAC	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACCTCTCCACATCAGCAGCTGTGCAACTCGAAGAT	243
Qy	241	TTTTCGAGTTTACTACTGTTCACAGAGTTTACACTACTTATATACCTTCGGGCCCTGGGACC	300
Db	244	TTTTCGAGTTTACTACTGTTCACAGAGTTTACAGTACCCCTTACACTTTTGGCCAGGGGACC	303
Qy	301	AAACTGGAGATCAAACTGA	318
Db	304	AAGCTGGAGATCAAACTGA	321

### RESULT 3

US-09-240-274-107 ; Sequence 107, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:

1. INVENTOR: Siegel, Donald L.  
2. APPLICANT: Siegel, Donald L.  
3. TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
4. TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
5. FILE REFERENCE: 09596-42U2  
6. CURRENT APPLICATION NUMBER: US/09/240,274  
7. CURRENT FILING DATE: 1999-01-29  
8. EARLIER APPLICATION NUMBER: 60/081,380  
9. EARLIER FILING DATE: 1998-04-10  
10. EARLIER APPLICATION NUMBER: 60/028,550  
11. EARLIER FILING DATE: 1996-10-11

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; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321

```

FEATURE: anti-Rh(D) chain I07  
OTHER INFORMATION: anti-Rh(D) chain I07  
US-09-240-274-107

Query Match	85.9%	Score 273.2;	DB 3;	Length 321;
Best Local Similarity	91.2%;	Pred. No. 2.6e-84;		
Matches 290; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0;

Qy	1	GAGCTCACCAAGTCTCCATCTCCTGTCCTGCTGTAGGACAGAGTGCACCATCACT	60
Db	4	GAGCTCACCAAGTCTCCATCTCCTGTCCTGCTGTAGGACAGAGTGCACCATCACT	63
Qy	61	TGCCGGGCAGCTCAGAGTATTAGCACCTATTAAATTGGTATCAGCAGAAACCGGGGAAG	120
Db	64	TGCCGGGCAGTTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCGGGAAA	123
Qy	121	GCCCTTAAGTCCTGATCTGTAGTCATCCCAATTTGCAAGTGGGCTCCCATCCAGGTTTC	180
Db	124	GCCCTTAAGTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGCTCCCATCAGGTTTC	183
Qy	181	AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACTGAAGAT	243
Qy	241	TTTTCAGATTACTACTGTCAACAGATTTACACTACTTTATATACCTTGGCCCTCGGACC	300
Db	244	TTTTCGAATTACTACTGTCAACAGATTTACAGTACCCCTCGCAACTTTGGCGGAGGACC	303
Qy	301	AAACTGGAGATCAAAACGA	318
Db	304	AAGGTGGAGATCAAAACGA	321

## RESULT 4

US-09-240-274-113  
; Sequence 113, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh (D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I13
US-09-240-274-113

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Query Match	85.9%	Score 273.2;	DB 3;	Length 321;
Best Local Similarity	91.2%	Pred. No. 2.6e-84;		
Matches 290; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0;

	Qy	1	GAGCTCACCCAGTCTCCATCCTCCGTGTCCTGTAGGACAGAGTCAACCATCACT	60
	Dd	4	GAGTTCACCCAGTCTCCATCCTCCGTGTCCTGTAGGACAGAGTCAACCATCACT	63
	Ov	61	TGCCGGGCACGCTCAGAGTATTAGCACCTATTAAAATTTGGTATCAGCAGAAAAACCGGGGAAG	120

Db 64 TGCCGGCAAGTCAGAGATTAGCAGGTATTAAATTGGTATCAGCAGAAACCCAGGAAA 123  
Qy 121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTGGCAAAGTGGGGTCCCAATCCAGGTTT 180  
Db 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCAATCAAGGTTT 183  
Qy 181 AGTGGCAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACCGTACCCTCAGAGTTTGGCCGGGGACC 303  
Qy 301 AAATGGAGATCAACGA 318  
Db 304 AAGCTGGAGATCAACGA 321

## RESULT 5

US-09-240-274-201  
; Sequence 201, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 201  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16  
US-09-240-274-201

Query Match 85.9%; Score 273.2; DB 3; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 1 GAGCTCACCCAGTCTCCATCTCCTCTGCTGCTCTGTAGGAGACAGATCACCATCACT 60  
Db 4 GAGCTCACCCAGTCTCCATCTCCTCTGCTGCTCTGTAGGAGACAGATCACCATCACT 63  
Qy 61 TGCCGGCAAGTCAGAGATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAA 120  
Db 64 TGCCGGCAAGTCAGAGATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCAGGAAA 123  
Qy 121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTGGCAAAGTGGGGTCCCAATCCAGGTTT 180  
Db 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCAATCAAGGTTT 183  
Qy 181 AGTGGCAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACAGTACCCTCAGAGTTTGGCCGGGGACC 303  
Qy 301 AAATGGAGATCAACGA 318  
Db 304 AAGCTGGAGATCAACGA 321

## RESULT 6

US-09-240-274-211  
; Sequence 211, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 211  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36  
US-09-240-274-211

Query Match 85.9%; Score 273.2; DB 3; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84;  
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 1 GAGCTCACCCAGTCTCCATCTCCTCTGCTGCTCTGTAGGAGACAGATCACCATCACT 60  
Db 4 GAGCTCACCTCAGTCTCCATCTCCTCTGCTGCTCTGTAGGAGACAGATCACCATCACT 63  
Qy 61 TGCCGGCAAGTCAGAGATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAA 120  
Db 64 TGCCGGCAAGTCAGAGATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCAGGAAA 123  
Qy 121 GCCCCTAAGCTCCTGATCTGTAGTGCATCCAAATTGGCAAAGTGGGGTCCCAATCCAGGTTT 180  
Db 124 TCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCAATCAAGGTTT 183  
Qy 181 AGTGGCAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCAACCTGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACAGTACCCTCAGAGTTTGGCCCTGGGACC 303  
Qy 301 AAATGGAGATCAACGA 318  
Db 304 AAGCTGGAGATCAACGA 321

## RESULT 7

US-09-240-274-218  
; Sequence 218, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 218

LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-240-274-218

Query Match 85.4%; Score 273.2; DB 3; Length 321;  
Best Local Similarity 91.2%; Pred. No. 2.6e-84; Indels 0; Gaps 0;  
Matches 290; Conservative 0; Mismatches 28;

QY 1 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTCTGTAGGACAGAGTCAACCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGGACAGAGTCAACCATCACT 63

QY 61 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 120  
DB 64 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 123

QY 121 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
DB 124 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 183

QY 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 184 AGTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 243

QY 241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
DB 244 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTCACCTTCGGCCCAAGGACA 303

QY 301 AAACCTGGAGATCAACGA 318  
DB 304 AAGGTGGAATCAACGA 321

RESULT 8  
US-09-240-274-106  
Sequence 106, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240, 274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 106  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I06  
US-09-240-274-106

Query Match 85.4%; Score 271.6; DB 3; Length 321;  
Best Local Similarity 90.9%; Pred. No. 9.1e-84; Indels 0; Gaps 0;  
Matches 289; Conservative 0; Mismatches 29;

QY 1 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTCTGTAGGACAGAGTCAACCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGGACAGAGTCAACCATCACT 63

QY 61 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 120  
DB 64 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 123

QY 121 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
DB 124 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 183

QY 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 184 AGTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 243

QY 241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
DB 244 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTCACCTTCGGCCCAAGGACA 303

QY 301 AAACCTGGAGATCAACGA 318  
DB 304 AAGGTGGAATCAACGA 321

RESULT 9  
US-09-240-274-205  
Sequence 205, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240, 274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 205  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH24  
US-09-240-274-205

Query Match 85.4%; Score 271.6; DB 3; Length 321;  
Best Local Similarity 90.9%; Pred. No. 9.1e-84; Indels 0; Gaps 0;  
Matches 289; Conservative 0; Mismatches 29;

QY 1 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTCTGTAGGACAGAGTCAACCATCACT 60  
DB 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGTAGGACAGAGTCAACCATCACT 63

QY 61 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 120  
DB 64 TCCCGGGCAGTCAAGATTTAGACCTATTAAATTTGGTATCAGCAGAAACCGGGGAG 123

QY 121 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 180  
DB 124 GCCCTAAGCTCCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTTC 183

QY 181 AGTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 240  
DB 184 ACTGCAGTGGATCTGGACAGAGTTCATCTCACCATCAGCAATCTGCAACCTGAAGAC 243

QY 241 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
DB 244 TTTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTCGTGGACGTTCCGCAAGGACC 303

QY 301 AAACCTGGAGATCAACGA 318  
DB 304 AAGGTGGAATCAACGA 321

RESULT 10  
US-09-240-274-221

; Sequence 221, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 221  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52  
US-09-240-274-221

Query Match 85.4%; Score 271.6; DB 3; Length 321;  
Best Local Similarity 90.9%; Pred. No. 9.1e-84;  
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 63  
Qy 61 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 120  
Db 64 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 123  
Qy 121 GCCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGTCCCAATCCAGGTTT 180  
Db 124 GCCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGTCCCAATCCAGGTTT 183  
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCAGCAATCTGCAACCTGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTCGGCCCTGGGACC 303  
Qy 301 AAAGTGGAGATCAAAACGA 318  
Db 304 AAGGTGGAATCAAAACGA 321

RESULT 11  
US-09-240-274-222  
; Sequence 222, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 222  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-240-274-222  
Query Match 85.4%; Score 271.6; DB 3; Length 321;  
Best Local Similarity 90.9%; Pred. No. 9.1e-84;  
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 63  
Qy 61 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 120  
Db 64 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 123  
Qy 121 GCCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGTCCCAATCCAGGTTT 180  
Db 124 GCCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGTCCCAATCCAGGTTT 183  
Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACCTGAAGAC 240  
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCAACATCAGCAATCTGCAACCTGAAGAT 243  
Qy 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGCCCTGGGACC 300  
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACCTTCGGCCCTGGGACC 303  
Qy 301 AAAGTGGAGATCAAAACGA 318  
Db 304 AAGGTGGAATCAAAACGA 321  
RESULT 12  
US-09-240-274-215  
; Sequence 215, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 215  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH46  
US-09-240-274-215

Query Match 84.9%; Score 270; DB 3; Length 321;  
Best Local Similarity 90.6%; Pred. No. 3.2e-83;  
Matches 288; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 1 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 60  
Db 4 GAGCTACCCAGTCTCCATCTCTGCTGCTCTCTGTAGGAGACAGAGTCAACATCACT 63  
Qy 61 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 120  
Db 64 TGCCGGGCAGTCTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCGGGAAG 123  
Qy 121 GCCCCTAAGCTCTCTGATCTGTAGTGCATCCAAATTGCAAAAGTGGGTCCCAATCCAGGTTT 180  
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US-09-472-087-62

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Query Match      84.1%; Score 267.4; DB 4; Length 714;
Best Local Similarity 90.2%; Pred. NO. 3.7e-82;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 2 AGCTCACCCAGTCTCCATCCCTGCTGCTGTAGGAGACAGAGTCACCATCACTT 61
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Db 74 AGATGACCCAGTCTCCATCCCTGCTGCTGTAGGAGACAGAGTCACCATCACTT 133
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Qy 62 GCCGGGCAAGTCAGAGTATTAGCACCTATTTAAATTGGTATCAGCAGAAACCGGGGAAG 121
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Db 134 GCCGGGCAAGTCAGAGTATTAGCACCTATTTAGATTGGTATCAGCAGAAACCGGGGAAG 193
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Qy 122 CCCCTAAGCTCCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCCATCCAGGTTCA 181
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Db 194 CCCCTAAGCTCCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCCATCAAGGTTCA 253
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Qy 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGACT 241
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Db 254 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCACTGCAACTGAAGATT 313
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Qy 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGGCCCTGGACCA 301
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Db 314 TTGCAAGTTACTACTGTCAACAGATTTACAGTACTCCATTCACTTGGCCCTGGACCA 373
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Qy 302 AACTGGAGATCAACGA 318
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OM nucleic - nucleic search, using sw model

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Title: US-10-027-725A-6

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Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

# SUMMARIES

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4	291.4	91.6	974	6	AX306529	AX306529 Sequence
5	291.4	91.6	974	6	BD131246	BD131246 Human mon
6	291	91.5	388	6	AR161375	AR161375 Sequence
7	291	91.5	388	6	AR369968	AR369968 Sequence
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9	289.8	91.1	327	9	HSA388657	AJ388657 Homo sapi
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11	289.2	90.9	324	9	AF306360	AF306360 Homo sapi
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14	288.2	90.6	812	9	AB064045	AB064045 Homo sapi
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19	285	89.6	330	9	AF240362	AF240362 Homo sapi
20	283.4	89.1	324	9	AB095282	AB095282 Homo sapi
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22	283.4	89.1	420	6	AR369974	AR369974 Sequence
23	283.4	89.1	420	6	BD096608	BD096608 Transgeni
24	283.4	89.1	3819	6	AR161402	AR161402 Sequence
25	283.4	89.1	3819	6	AR369997	AR369997 Sequence
26	283.4	89.1	3819	6	BD096631	BD096631 Transgeni
27	280.8	88.3	728	6	AX327729	AX327729 Sequence
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29	280.4	88.2	321	6	AX365137	AX365137 Sequence
30	278.6	87.6	324	9	AB063969	AB063969 Homo sapi
31	278.6	87.6	326	9	AF103397	AF103397 Homo sapi
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35	277	87.1	439	6	AR161377	AR161377 Sequence
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38	275.4	86.6	324	9	AB095289	AB095289 Homo sapi
39	275.4	86.6	384	6	I27685	I27685 Sequence 13
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42	275.2	86.5	312	9	HSX98967	X98967 H.sapiens r
43	274.8	86.4	324	9	AB095284	AB095284 Homo sapi
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# ALIGNMENTS

RESULT 1  
HSA458381  
LOCUS  
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain  
variable region (IGKV gene), clone 100.  
ACCESSION AJ458381  
VERSION AJ458381.1 GI:20387061  
KEYWORDS IGV gene; immunoglobulin kappa; light chain; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
1  
Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y.,  
Valent P., Kraft D. and Valenta R.

Pred. No. is the number of results predicted by chance to have a

TITLE Conversion of grass allergen-specific human IgE into a protective  
JOURNAL IGE antibody  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 318)  
TITLE Flicker, S.  
JOURNAL Direct Submission  
SUBMITTED (24-APR-2002) Flicker S., Department of Pathophysiology,  
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090  
Vienna, AUSTRIA

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ORIGIN  
Query Match 100.0%; Score 318; DB 9; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.4e-89;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCTCAGCAGTCTCCATCTTCCTGTCATCTGATGAGGACAGAGTACCATAACT 60  
Db 1 GAGCTCAGCAGTCTCCATCTTCCTGTCATCTGATGAGGACAGAGTACCATAACT 60  
QY 61 TGTGGGGAGTTCAGGCTATTAGCAGTTGGTTAGCTGCTGATCAGCAGAAACCGAGAAA 120  
Db 61 TGTGGGGAGTTCAGGCTATTAGCAGTTGGTTAGCTGCTGATCAGCAGAAACCGAGAAA 120  
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Db 241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
QY 301 AAGGTGGAATCAACGA 318  
Db 301 AAGGTGGAATCAACGA 318

RESULT 2  
H5IGKLC5  
LOCUS H5IGKLC5 705 bp RNA linear SYN 29-MAR-2001  
DEFINITION Synthetic construct including Homo sapiens immunoglobulin kappa  
chain (clone: 5).  
ACCESSION X95747  
VERSION X95747.1 GI:1514580  
KEYWORDS constant region; immunoglobulin; kappa light chain.  
SOURCE synthetic construct  
ORGANISM synthetic construct

artificial sequences.  
1 Steinberger, P., Kraft, D. and Valenta, R.  
Construction of a combinatorial IGE library from an allergic  
patient. Isolation and characterization of human IGE Fabs with  
specificity for the major timothy grass pollen allergen, phi p 5  
J. Biol. Chem. 271 (18), 10967-10972 (1996)  
96210038  
MEDLINE  
PUBMED 8631916  
2 (bases 1 to 705)  
Valenta, R.L.S.  
Direct Submission  
TITLE Submitted (19-FEB-1996) R.L.S. Valenta, Institute of General &  
JOURNAL Experimental Pathology, General Hospital, Waehringer Guertel 18-20,  
1090 Vienna, AUSTRIA  
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67..72  
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163..207  
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 QY 182 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
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 QY 302 AGGTGGAATCAAAACA 318  
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 Db 412 AGGTGGAATCAAAACA 428  
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RESULT 5  
 BD131246 974 bp DNA linear PAT 18-SEP-2002  
 LOCUS Human monoclonal antibody against constimulation transducer  
 DEFINITION molecule ALLIM and medicinal utilization thereof.  
 ACCESSION BD131246  
 VERSION JP 2002034581-A/28.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Tsuji,T., Tezuka,K. and Hori,N.  
 TITLE Human monoclonal antibody against constimulation transducer  
 molecule ALLIM and medicinal utilization thereof  
 JOURNAL Patent: JP 2002034581-A 28 05-FEB-2002;  
 JAPAN TOBACCO INC

COMMENT OS Homo sapiens (human)  
 PN JP 2002034581-A/28  
 PD 05-FEB-2002  
 PF 30-MAR-2001 JP 2001099508  
 PI TAKASHI TSUIJI,KATSUNARI TEZUKA,NOBUAKI HORI  
 PC C12N15/09,A61K31/7088,A61K38/00,A61K39/395,A61K45/  
 PC 00,A61P37/08,  
 PC A61P43/00,A61P43/00,C07K16/28,C07K16/46,C07K19/00,C12N5/10, PC  
 C12N15/02,  
 PC C12P21/08,G01N33/15,G01N33/50,G01N33/53,G01N33/566,G01N33/577// PC  
 (C12P21/08,C12R1:91),C12N15/00,A61K37/02,C12N5/00,C12N15/00 CC  
 Human monoclonal antibody against constimulation transducer CC  
 molecule ALLIM

CC and medicinal utilization thereof  
 FH Key Location/Qualifiers  
 FT 5'UTR (1)..(38)  
 FT CDS (39)..(749)  
 FT 3'UTR (750)..(974)  
 FT sig\_peptide (39)..(104).  
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 Best Local Similarity 95.0%; Pred. No. 5.6e-81;  
 Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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 QY 62 GTCGGCGAGTCAGGCTATAGCAGTTGGTTAGCCTGGTATCAGCAGAAACAGGGGAAG 121  
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 Db 172 GTCGGCGAGTCAGGCTATAGCAGTTGTTAGCCTGGTATCAGCAGAAACAGGGGAAG 231  
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 QY 182 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
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 QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
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 Db 352 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTGGACGTTTCGGCCAGGGGACCA 411  
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 QY 302 AGGTGGAATCAAAACA 318  
 |||||  
 Db 412 AGGTGGAATCAAAACA 428  
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RESULT 6  
 AR161375 388 bp DNA linear PAT 17-OCT-2001  
 LOCUS Sequence 358 from patent US 6255458.  
 DEFINITION AR161375  
 ACCESSION AR161375  
 VERSION AR161375.1 GI:16227235  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 388)  
 AUTHORS Lonberg,N. and Kay,R.M.  
 TITLE High affinity human antibodies and human antibodies against digoxin  
 JOURNAL Patent: US 6255458-A 358 03-JUL-2001;  
 FEATURES Location/Qualifiers  
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ORIGIN  
 Query Match 91.5%; Score 291; DB 6; Length 388;  
 Best Local Similarity 95.2%; Pred. No. 8.4e-81;  
 Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTCTCCGTGTCGTGATCTGTAGGACAGAGTCACCAATACTT 61  
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 QY 62 GTCGGCGAGTCAGGCTATAGCAGTTGGTTAGCCTGGTATCAGCAGAAACAGGGGAAG 121  
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 Db 134 GTCGGCGAGTCAGGCTATAGCAGTTGGTTAGCCTGGTATCAGCAGAAACAGGGGAAG 193  
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 Db 194 CCCCTAAAGTCTGATCTATGCTGATCCAGTTTCGAAAGTGGGTCCCGTCAAGGTTCA 253  
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 QY 182 GCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
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 QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
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 Db 314 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373  
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 QY 302 AGGTGGAATCAAAACA 316  
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 Db 374 AGGTGGAATCAAAACA 388  
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RESULT 7  
 AR369968 388 bp DNA linear PAT 12-SEP-2003  
 LOCUS Sequence 206 from patent US 6300129.  
 DEFINITION AR369968  
 ACCESSION AR369968  
 VERSION AR369968.1 GI:34606409



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ORIGIN  
Query Match 91.1%; Score 289.8; DB 9; Length 327;  
Best Local Similarity 94.6%; Pred. No. 2.1e-80;  
Matches 300; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
  
QY 2 AGCTCACGAGTCTCCATCTTCCGTGTCGTAGGACAGAGTCAACCAATCTT 61  
Db |||||  
8 AGATGACCCAGTCTCCATCTTCCGTGTCGTAGGACAGAGTCAACCAATCTT 67  
QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCAGGACAGAAACAGGGAAG 121  
Db |||||  
68 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCAGGACAGAAACAGGGAAG 127  
QY 122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTCGAAAGTGGGTCCCGTCAAGGTTCA 181  
Db |||||  
128 CCCCTAAGCTCTGATCTATTCTGCATCCAGTTTCGAAAGTGGGTCCCGTCAAGGTTCA 187  
QY 182 GCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGGCTGAAGATT 241  
Db |||||  
188 GCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGGCTGAAGATT 247  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db |||||  
248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 307  
QY 302 AGGTGGAATCAACCA 318  
Db |||||  
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RESULT 10  
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LOCUS Homo sapiens MCL047 immunoglobulin light chain variable region  
DEFINITION mRNA, partial cds.  
ACCESSION AY043120  
VERSION AY043120.1 GI:18025629  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,  
Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.  
TITLE Ig VL gene repertoire in B cell type chronic lymphocytic leukemia  
JOURNAL Unpublished  
AUTHORS  
2 (bases 1 to 322)  
Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,  
Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350  
Community Drive, Manhasset, NY 11030, USA
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CDS

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## ORIGIN

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Best Local Similarity 94.9%; Pred. No. 2.8e-80;  
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QY 2 AGCTCACGAGTCTCCATCTTCCGTGTCGTAGGACAGAGTCAACCAATCTT 61  
Db |||||  
8 AGATGACCCAGTCTCCATCTTCCGTGTCGTAGGACAGAGTCAACCAATCTT 67  
QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCAGGACAGAAACAGGGAAG 121  
Db |||||  
68 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTCAGGACAGAAACAGGGAAG 127  
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Db |||||  
128 CCCCTAAGCTCTGATCTATTCTGCATCCAGTTTCGAAAGTGGGTCCCGTCAAGGTTCA 187  
QY 182 GCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGGCTGAAGATT 241  
Db |||||  
188 GCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAGGCTGAAGATT 247  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db |||||  
248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 307  
QY 302 AGGTGGAATCAAC 316  
Db |||||  
308 AGGTGGAATCAAC 322
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RESULT 11  
AF306360

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LOCUS Homo sapiens clone TF2.4 immunoglobulin light chain variable region  
DEFINITION mRNA, partial cds.  
ACCESSION AF306360  
VERSION AF306360.1 GI:14573216  
KEYWORDS  
SOURCE Homo sapiens (human)
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## ORGANISM

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Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Pichurin,P., Guo,J., Yan,X., Rapoport,B. and McLachlan,S.M.  
TITLE Human monoclonal autoantibodies to B-cell epitopes outside the  
thyroid peroxidase autoantibody immunodominant region  
JOURNAL Thyroid 11 (4), 301-313 (2001)  
AUTHORS  
2 (bases 1 to 324)  
McLachlan,S.M., Rapoport,B., Pichurin,P., Guo,J. and Yan,X.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-2000) Medicine, Cedars-Sinai Medical Center, 8700  
Beverly Blvd, B-131, Los Angeles, CA 90048, USA
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## FEATURES

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CDS

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QY 181 AGCGCAGTGGATCTGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGAT 240
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QY 241 TCTGCACTTACTATTGTCAACAGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
Db 247 TTTGCACTTACTATTGTCAACAGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 306
QY 301 AAGGTGGAATCAACGA 318
Db 307 AAGGTGGAATCAACGA 324

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RESULT 12
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LOCUS
DEFINITION Homo sapiens antibody light chain variable region (EL-14) mRNA,
partial cds.
ACCESSION AF146407
VERSION AF146407.1 GI:5081718
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
van Den Brink,E.N., Turenhout,E.A., Davies,J., Bovenschen,N.,
Fijnvandraat,K., Ouwehand,W.H., Peters,M. and Voorberg,J.
Human antibodies with specificity for the C2 domain of factor VIII
are derived from VHI germline genes
JOURNAL Blood 95 (2), 558-563 (2000)
MEDLINE 20094679
PUBMED 10627462
REFERENCE 2 (bases 1 to 324)
AUTHORS van den Brink,E.N. and Voorberg,J.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1999) Blood Coagulation, CLB, Sanguin Blood
Supply Foundation, Plesmanlaan 125, Amsterdam 1066 CX, The
Netherlands

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CDS

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Best Local Similarity 94.3%; Pred. No. 6.6e-80;
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTCCATCTTCGGTGCTGTCATCTGTAGGAGACAGAGTCACCATAACT 60
Db 7 GTGTAGACCCAGTCTCCATCTTCGGTGCTGTCATCTGTAGGAGACAGAGTCACCATCACT 66
QY 61 TGTGGGCGAGTCAGGATATTAGCAGTGGTTAGCTGGTATCAGCAGAAACCCAGGGAAA 120
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QY 121 GCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAGTGGGGTCCCGTCAAGGTTTC 180
Db 127 GCCCTAAGCTCCTGATCTATTCTGCATCCAGTTTGCAAGTGGGGTCCCGTCAAGGTTTC 186
QY 181 AGCGCAGTGGATCTGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGAT 240
Db 187 AGCGCAGTGGATCTGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGAT 246
QY 241 TCTGCACTTACTATTGTCAACAGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
Db 247 TTTGCACTTACTATTGTCAACAGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 306
QY 301 AAGGTGGAATCAACAG 317
Db 307 AAGGTGGAATCAACAG 323

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RESULT 13
S59162
LOCUS
DEFINITION Ig V kappa -anti-single/double-stranded DNA antibody NE-13 light
chain variable region [human, B-cells, mRNA partial, 433 nt].
ACCESSION S59162
VERSION S59162.1 GI:2999955
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hirabayashi,Y., Munakata,Y., Takai,O., Shibata,S., Sasaki,T. and
Sano,H.
Human B-cell clones expressing lupus nephritis-associated anti-DNA
idiotypes are preferentially expanded without somatic mutation
JOURNAL Scand. J. Immunol. 37 (5), 533-540 (1993)
MEDLINE 93248539
PUBMED 8387226
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 130630] from the original journal article.
This sequence comes from Fig. 6.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 318

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vit.\*

21: em\_gss\_fun.\*

22: em\_gss\_man.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gsst.\*

29: gb\_gsst.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294.6	92.6	943	10 BF976230	BF976230 602245105
2	289.8	91.1	891	13 BX336281	BX336281 BX336281
3	288.2	90.6	554	10 BE939490	BE939490 QV0-UM009
4	286.6	90.1	1100	10 BF663472	BF663472 602144635

5	285	89.6	606	14	CD690290	CD690290 EST6813 h
6	283.4	89.1	558	14	CD690030	CD690030 EST6553 h
7	283.4	89.1	755	12	BG533970	BG533970 602553071
8	283.4	89.1	997	13	BX336280	BX336280 BX336280
9	282	88.7	605	14	CD688415	CD688415 EST4937 h
10	281.8	88.6	472	14	CD702614	CD702614 EST19139
11	280.2	88.1	497	14	CD696718	CD696718 EST13241
12	278.6	87.6	912	10	BF129120	BF129120 601811580
13	276.2	86.9	894	12	BG341803	BG341803 602463535
14	275.4	86.6	561	14	CD706288	CD706288 EST22815
15	274.6	86.4	851	12	BG686018	BG686018 602638582
16	272	85.5	629	14	CD697149	CD697149 EST13672
17	271.4	85.3	421	14	CD690477	CD690477 EST7000 h
18	270.6	85.1	459	14	CD695600	CD695600 EST12123
19	268.8	84.5	903	13	BQ706785	BQ706785 AGENCOURT
20	267.2	84.0	710	14	CD695065	CD695065 EST11588
21	266.6	83.8	906	12	BG756264	BG756264 602713576
22	265.8	83.6	484	14	CD696042	CD696042 EST12565
23	265.8	83.6	486	14	CD683960	CD683960 EST480 hu
24	265.8	83.6	487	10	AW405988	AW405988 UT-HF-BL0
25	265.8	83.6	594	12	BI001311	BI001311 MR2-HN006
26	264.2	83.1	724	12	BI837410	BI837410 603086702
27	264.2	83.1	421	10	AW406227	AW406227 UT-HF-BL0
28	264.2	83.1	510	14	CD694557	CD694557 EST11080
29	264.2	83.1	594	10	AW380184	AW380184 QV3-HT026
30	264.2	83.1	769	14	CB957759	CB957759 AGENCOURT
31	264.2	83.1	886	12	BG756818	BG756818 602710291
32	263.2	82.8	612	14	CB553710	CB553710 MMSP0024
33	262.6	82.6	545	14	CD697196	CD697196 EST13719
34	262.6	82.6	677	14	CD692170	CD692170 EST8709 h
35	262.6	82.6	748	14	CB956867	CB956867 AGENCOURT
36	262.6	82.6	759	14	CB984469	CB984469 AGENCOURT
37	261	82.1	422	10	AW407904	AW407904 UT-HF-BL0
38	261	82.1	741	14	CB958688	CB958688 AGENCOURT
39	261	82.1	969	13	BU899279	BU899279 AGENCOURT
40	259.4	81.6	447	10	AW405752	AW405752 UT-HF-BL0
41	259.4	81.6	689	14	CB055233	CB055233 NTSC_gm08
42	259.4	81.6	867	12	BG754732	BG754732 602714301
43	258.4	81.3	834	12	BG679628	BG679628 602627680
44	257.8	81.1	493	10	AW405753	AW405753 UT-HF-BL0
45	257.8	81.1	525	14	CD705928	CD705928 EST22455

## ALIGNMENTS

RESULT 1  
BF976230  
LOCUS 602245105F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4336225 5', linear EST 22-JAN-2001  
DEFINITION 943 bp mRNA  
ACCESSION BF976230  
VERSION BF976230.1 GI:12343445  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 943)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-i@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L1CML208 row: j column: 02  
High quality sequence stop: 721.



Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel.: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-QV0-UM0093-250>)

Seq primer: puc 18 forward  
High quality sequence start: 21  
High quality sequence stop: 547.

## FEATURES

source

1..554

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="UM0093"

/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 90.6%; Score 288.2; DB 10; Length 554;

Best Local Similarity 94.3%; Pred. No. 2.2e-80;

Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      2 AGCTCAGCAGCTCCATCTTCCTCGTCTGTCATCTGTAGGAGACAGATCCACATACTT 61
Db      36 AGATGACCCAGTCCCATCTTCCTCGTCTGTCATCTGTAGGAGACAGATCCACATACTT 95

Qy      62 GTCGGGGGAGTCAGGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 121
Db      96 GTCGGGGGAGTCAGGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 155

Qy      122 CCCCTAAACTCCTGATCTATTCTGATCCAGTTTGCAGTTGGGGTCCCGTCAAAGTTCA 181
Db      156 CCCCTAAAGTCTCTGATCTATGTCGATCCAGTTTGCAGTTGGGGTCCCGTCAAAGTTCA 215

Qy      182 GCGCAGTGGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGATT 241
Db      216 GCGCAGTGGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGATT 275

Qy      242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db      276 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 335

Qy      302 AGTGGAAATCAACGA 318
Db      336 AGCTGGAGATCAACGA 352

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## RESULT 4

BF663472

LOCUS 602144635F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4297736 5', mRNA sequence.

DEFINITION BF663472.1 GI:11937367

ACCESSION BF663472

VERSION BF663472.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1100)

NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CMI152 row: f column: 09

High quality sequence stop: 704.

## FEATURES

source

1..1100

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="IMAGE:4297736"

/tissue\_type="Primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected &gt;500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 90.1%; Score 286.6; DB 10; Length 1100;

Best Local Similarity 94.0%; Pred. No. 1.1e-79;

Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy      2 AGCTCAGCAGCTCCATCTTCCTCGTCTGTCATCTGTAGGAGACAGATCCACATACTT 61
Db      81 AGATGACCCAGTCCCATCTTCCTCGTCTGTCATCTGTAGGAGACAGATCCACATACTT 140

Qy      62 GTCGGGGGAGTCAGGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 121
Db      141 GTCGGGGGAGTCAGGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 200

Qy      122 CCCCTAAACTCCTGATCTATTCTGATCCAGTTTGCAGTTGGGGTCCCGTCAAAGTTCA 181
Db      201 CCCCTAAAGTCTCTGATCTATGCTTCATCCAGTTTGCAGTTGGGGTCCCGTCAAAGTTCA 260

Qy      182 GCGCAGTGGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTCAAGATT 241
Db      261 GCGCAGTGGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTCAAGATT 320

Qy      242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db      321 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 380

Qy      302 AGTGGAAATCAACGA 318
Db      381 AGTGGAGATCAACGA 397

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## RESULT 5

CD690290

LOCUS

DEFINITION EST6813 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD690290

VERSION CD690290.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 606)

AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.  
Transcriptional Gene Expression Profile of Human Nasopharynx  
Unpublished (2003)  
Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

FEATURES  
source  
1. .606  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cdna library from southern Chinese"

ORIGIN  
Query Match 89.6%; Score 285; DB 14; Length 606;  
Best Local Similarity 93.7%; Pred. No. 2.4e-79;  
Matches 297; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACCAATCTT 61  
DB 141 AGATGACCCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACCAATCTT 200

QY 62 GTCGGCGAGTCAGGATTTAGCAGTTGGTTCAGCTGTAGCTGATCAGCAGAAACAGGGAAG 121  
DB 201 GTCGGCGAGTCAGGATTTAGCAGTTGGTTCAGCTGTAGCTGATCAGCAGAAACAGGGAAG 260

QY 122 CCCCTAACTCCTGATCTATTCTGTCATCCAGTTTGCAGTTTGCAGTTTCCCGTCAAGTTCA 181  
DB 261 CCCCTAACTCCTGATCTATGTCATCCAGTTTGCAGTTTGCAGTTTCCCGTCAAGTTCA 320

QY 182 GCGGAGTGGATCTGGGACAGATTTAGCTCAGCTGATCAGCAGCTGAGCTGAGATT 241  
DB 321 GCGGAGTGGATCTGGGACAGATTTAGCTCAGCTGATCAGCAGCTGAGCTGAGATT 380

QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
DB 381 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 440

QY 302 AGGTGGAATCAACGA 318  
DB 441 AGGTGGAATCAACGA 457

RESULT 6  
CD690030  
LOCUS  
DEFINITION  
EST6553 human nasopharynx Homo sapiens cdna, mRNA sequence.  
ACCESSION  
CD690030  
VERSION  
CD690030.1 GI:32210387  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 558)  
AUTHORS  
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
REFERENCE  
Transcriptional Gene Expression Profile of Human Nasopharynx  
Unpublished (2003)  
Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

Zeng, Y.-X.  
Transcriptional Gene Expression Profile of Human Nasopharynx  
Unpublished (2003)  
Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

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Location/Qualifiers  
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/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cdna library from southern Chinese"

ORIGIN  
Query Match 89.1%; Score 283.4; DB 14; Length 558;  
Best Local Similarity 93.4%; Pred. No. 7.3e-79;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACCAATCTT 61  
DB 123 AGATGACCCAGTCTCCATCTTCGGTCTGTCATCTGTAGGAGACAGAGTCACCAATCTT 182

QY 62 GTCGGCGAGTCAGGATTTAGCAGTTGGTTCAGCTGTAGCTGATCAGCAGAAACAGGGAAG 121  
DB 183 GTCGGCGAGTCAGGATTTAGCAGTTGGTTCAGCTGTAGCTGATCAGCAGAAACAGGGAAG 242

QY 122 CCCCTAACTCCTGATCTATTCTGTCATCCAGTTTGCAGTTTGCAGTTTCCCGTCAAGTTCA 181  
DB 243 CCCCTAACTCCTGATCTATGTCATCCAGTTTGCAGTTTGCAGTTTCCCGTCAAGTTCA 302

QY 182 GCGGAGTGGATCTGGGACAGATTTAGCTCAGCTGATCAGCAGCTGAGCTGAGATT 241  
DB 303 GCGGAGTGGATCTGGGACAGATTTAGCTCAGCTGATCAGCAGCTGAGCTGAGATT 362

QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
DB 363 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 422

QY 302 AGGTGGAATCAACGA 318  
DB 423 AGGTGGAATCAACGA 439

RESULT 7  
BG533970  
LOCUS  
DEFINITION  
mRNA sequence.  
ACCESSION  
BG533970.1 GI:13525510  
VERSION  
BG533970.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 755)  
AUTHORS  
NIH-MGC http://mgc.mci.nih.gov/.  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCMI484 row: m column: 17  
High quality sequence stop: 726.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4663096"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 77"  
/note="organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcccttggcc); Site 2: SfiI (ggccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCCATTAAGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 89.1%; Score 283.4; DB 12; Length 755;  
Best Local Similarity 93.4%; Pred. No. 8.8e-79;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 2 AGCTCACGAGTCTCCATCTTCCTGCTGCTAGGAGACAGAGTACCATACTT 61  
Db |||||  
101 AGATGACCCAGTCTCCATCTTCCTGCTGCTAGGAGACAGAGTACCATACTT 160  
Qy 62 GTCGGCGAGTCAAGGTATTAGAGTTGGTTAGCTGCTATCAGCAGAAACACGGAAG 121  
Db |||||  
161 GTCGGCGAGTCAAGGTATTAGAGTTGGTTAGCTGCTATCAGCAGAAACACGGAAG 220  
Qy 122 CCCCTAACTCTGATCTATTCGATCCAGTTGCAAGTGGGTCCCGTCAAGTTCA 181  
Db |||||  
221 CCCCTAACTCTGATCTATTCGATCCAGTTGCAAGTGGGTCCCGTCAAGTTCA 280  
Qy 182 GCGGCGAGTGGATCGGACAGATTTCAGTCCACCATCAGCAGCTGCGAGCTGAAGATT 241  
Db |||||  
281 GCGGCGAGTGGATCGGACAGATTTCAGTCCACCATCAGCAGCTGCGAGCTGAAGATT 340  
Qy 242 CTGCAACTTACTATGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db |||||  
341 TTGCAACTTACTATGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 400  
Qy 302 AGTGGAATCAACGA 318  
Db |||||  
401 AGTGGAATCAACGA 417

RESULT 8  
BX336280/c  
LOCUS BX336280 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CSODI026YL22 3-PRIME, mRNA sequence.  
ACCESSION BX336280  
VERSION BX336280.1 GI:30339485  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 997)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 1696.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODI026DF11NP1&cluster=1696.r. Contact :  
Feng Liang Email: fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODI026DF11NP1.  
FEATURES  
Location/Qualifiers  
1. .997  
source

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/clone="CSODI026YL22"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 89.1%; Score 283.4; DB 13; Length 997;  
Best Local Similarity 92.4%; Pred. No. 1e-78;  
Matches 293; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 2 AGCTCACGAGTCTCCATCTTCCTGCTGCTAGGAGACAGAGTACCATACTT 61  
Db |||||  
935 AGATGACCCAGTCTCCATCTTCCTGCTGCTAGGAGACAGAGTACCATACTT 876  
Qy 62 GTCGGCGAGTCAAGGTATTAGAGTTGGTTAGCTGCTATCAGCAGAAACACGGAAG 121  
Db |||||  
875 GTCGGCGAGTCAAGGTATTAGAGTTGGTTAGCTGCTATCAGCAGAAACACGGAAG 816  
Qy 122 CCCCTAACTCTGATCTATTCGATCCAGTTGCAAGTGGGTCCCGTCAAGTTCA 181  
Db |||||  
815 CCCCTAACTCTGATCTATTCGATCCAGTTGCAAGTGGGTCCCGTCAAGTTCA 756  
Qy 182 GCGGCGAGTGGATCGGACAGATTTCAGTCCACCATCAGCAGCTGCGAGCTGAAGATT 241  
Db |||||  
755 GCGGCGAGTGGATCGGACAGATTTCAGTCCACCATCAGCAGCTGCGAGCTGAAGATT 696  
Qy 242 CTGCAACTTACTATGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db |||||  
695 TTGCAACTTACTATGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 636  
Qy 302 AGTGGAATCAACGA 318  
Db |||||  
635 AGTGGAATCAACGA 619

RESULT 9  
CD688415  
LOCUS CD688415  
DEFINITION EST4937 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD688415  
VERSION CD688415.1 GI:32207195  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 605)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: YiXin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.  
FEATURES  
Location/Qualifiers  
1. .605  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue type="normal nasopharynx"  
/clone lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA  
library from southern Chinese"

	QY	62	GTCCGGCAGTCTGAGTTATAGCAGTTGGTTACCTTGTTATCATGACAGAAACCACCGGAAG	121
	Db	185	GTCCGGCAGTCTGAGTTATAGCAGTTGGTTACCTTGTTATCATGACAGAAACCACCGGAAG	244
	QY	122	CCCTTAACCTTCCTGCATCTATTCTTCATCCAGTTTGCAAGTGGGGTCCCCTCAAGTTCA	181
	Db	245	CCCCAAGCTCTCTGATCTATCTACTGATCCAGTTTGCAAGTGGGGTCCCCTCAAGTTCA	304
	QY	182	GCAGCAGTGTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCTTGAAGATT	241
	Db	305	GCAGCAGTGTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCTTGAAGATT	364
	QY	242	CTCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGGACCA	301
	Db	365	TTCGAATCTACTATGTCTACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGGACCA	424
	QY	302	AGGTGGAAATCAAACA	318
	Db	425	AGGTGGAGATCAAACA	441
	RESULT 11			
	CD96718		497 bp	mRNA linear EST 25-JUN-2003
	LOCUS	EST13241	human nasopharynx Homo sapiens	cDNA, mRNA sequence.
	DEFINITION	CD96718		
	ACCESSION	CD96718.1	GI:32223477	
	VERSION	EST.	Homo sapiens (human)	
	KEYWORDS		Homo sapiens	
	SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	REFERENCE		Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.	
	AUTHORS		Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)	
	JOURNAL		Contact: YiXin Zeng	
	COMMENT		Cancer Center	
	FEATURES		Sun Yat-sen University	
	source		651 Dongfeng Road East, Guangzhou 510060, China	
			Tel.: 86-1380-9770-743	
			Fax: 86-20-8775-4506	
			Email: yxzeng@gzsums.edu.cn.	
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			/mol_type="mRNA"	
			/db_xref="taxon:9606"	
			/tissue_type="normal nasopharynx"	
			/clone_lib="human nasopharynx"	
			/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"	
	ORIGIN			
	Query Match		88.1%; Score 280.2; DB 14; Length 497;	
	Best Local Similarity		92.7%; Pred. No. 7.1e-78;	
	Matches		294; Conservative 0; Mismatches 23; Indels 0; Gaps 0;	
	QY	2	AGCTCAGCAGTCTCCATCTTCCGTCTGTCATCTGTAGGACAGAGTCAACATACTT	61
	DB	120	AGATGCCAGTCTCCATCTTCCGGTCTGCTCTGTAGGACAGAGTCAACATACTT	179
	QY	62	GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACCAGGGAAG	121
	DB	180	GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACCAGGGAAG	239
	QY	122	CCCCTAACCTTCATCTTCTGCATCCAGTTTGCAAGTGGGGTCCCCTCAAGTTCA	181
	DB	240	CCCCTAAGCTCCTCGTCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCCTCAAGTTCA	299
	QY	182	CGCGCAGTGTGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCTTGAAGATT	241
ORIGIN				
Query Match			88.6%; Score 281.8; DB 14; Length 472;	
Best Local Similarity			93.1%; Pred. No. 2.1e-78;	
Matches			295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	
QY		2	AGCTCAGCAGTCTCCATCTTCCGTCTGTCATCTGTAGGACAGAGTCAACATACTT	61
DB		125	AGATGCCAGTCTCCATCTTCCGTCTGTCATCTGTAGGACAGAGTCAACATACTT	184



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Db      300 GCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 359
Qy      242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACACTTTTGGCCAGGGACCA 301
Db      360 TTGCAACTTACTATGTTCAACAGGCTAACAGTTTCCCTTTCACTTTTCGGCCCTGGGACCA 419
Qy      302 AGGTGGAATCAAAACGA 318
Db      420 AAGTGGATATCAACGA 436

RESULT 12
LOCUS   BF129120
DEFINITION 601811580F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:405430 5',
mRNA sequence.
VERSION  BF129120
KEYWORDS EST.
SOURCE   BF129120.1 GI:10968160
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM894 row: p column: 19
High quality sequence stop: 695.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:405430"
                     /tissue_type="Primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCAGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

ORIGIN
Query Match      87.6%; Score 278.6; DB 10; Length 912;
Best Local Similarity 92.4%; Pred. No. 3.3e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy      62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCCTGTGATACAGAGAAACCGGGAAG 121
Db      132 GTCGGGCGAGTCAGGATATTAGTAGTTGGTTAGCCTGTGATACAGAGAAACCGGGAAG 191
Qy      122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCGCCGTCAGGTTCA 181
Db      192 CCCCTAAACTCTGATCTATGCTGCATCCAGTTTACAAAGTGGGTCGCCATCAGGTTCA 251

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Qy      182 GCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241
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Qy      242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCACACTTTTGGCCAGGGACCA 301
Db      312 TTGCAACTTACATTTGTCTACAGACTAACAGTTTCCCATTCACTTTTCGGCCCTGGGACCA 371
Qy      302 AGGTGGAATCAAAACGA 318
Db      372 AAGTGGATATCAACGA 388

RESULT 13
LOCUS   BG341803
DEFINITION 602463535F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576136 5',
mRNA sequence.
ACCESSION BG341803
VERSION   BG341803
KEYWORDS  EST.
SOURCE    BG341803.1 GI:13148241
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1288 row: f column: 09
High quality sequence stop: 636.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4576136"
                     /tissue_type="Primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCAGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

ORIGIN
Query Match      86.9%; Score 276.2; DB 12; Length 894;
Best Local Similarity 94.0%; Pred. No. 1.9e-76;
Matches 298; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Qy      2 AGCTCAGCAGTCTCCATCTTCCTGCTGCTGCATCTGTAGGAGACAGATCCACCATACTT 61
Db      86 AGATGACCCAGTCTCCATCTTCCTGCTGCTGCATCTGTAGGAGACAGATCCACCATACTT 145
Qy      62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCCTGTGATACAGAGAAACCGGGAAG 121
Db      146 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCCTGTGATACAGAGAAACCGGGAAG 204

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 Db 265 GCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGATT 324  
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 QY 242 CTGCACTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
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 QY 302 AGGTGGAATCAACGA 318  
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 Db 385 AAGTGATATCAACGA 401  
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RESULT 14  
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 LOCUS EST22815 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD706288  
 ACCESSION CD706288.1 GI:32236918  
 VERSION EST.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 561)  
 AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and  
 Zeng,Y.-X.  
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Yixin Zeng  
 Cancer Center  
 Sun Yat-sen University  
 651 Dongfeng Road East, Guangzhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn.

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 Best Local Similarity 91.8%; Pred. No. 2.6e-76;  
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 Db 117 AGATGACCAAGTCTCCATCTCCGTCTGTCATCTGTAGAGACAGAGTCAACATAACTT 176  
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 QY 62 GTCCGCGAGTCAAGGTATTAGCAGTTGGTTAGCTTGTATCAGCAGAAACAGGGGAAAG 121  
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 Db 177 GTCCGCGAGTCAAGGTATTAGCAGTTGGTTAGCTTGTATCAGCAGAAACAGGGGAAAG 236  
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 QY 122 CCCTAACTCTGATCTATTCGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGGTTCA 181  
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 QY 182 GCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGATT 241  
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 Db 297 GCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGATT 356  
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 QY 242 CTGCAACTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
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Db 357 TTCAACTACTCTTGTGACGACAGTAAACAGTTTCCCTCGCACATTCGGCCAAAGGACCA 416  
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 QY 302 AGGTGGAATCAACGA 318  
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 Db 417 AGGTGGAATCAACGA 433  
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 RESULT 15  
 BG686018 851 bp mRNA linear EST 01-MAY-2001  
 LOCUS 602638582F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:476157 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG686018  
 VERSION BG686018.1 GI:13917415  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 851)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCW1626 row: c column: 22  
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 /note="Organ: B-cells; Vector: pOT7; Site:1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 86.4%; Score 274.6; DB 12; Length 851;  
 Best Local Similarity 93.7%; Pred. No. 5.9e-76;  
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 QY 122 CCCTAACTCTGATCTATTCGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGGTTCA 181  
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 Db 200 CCCTAACTCTGATCTATTCGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGGTTCA 259  
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 QY 182 GCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGATT 241  
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 Db 260 GCGGCAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGATT 319  
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Qy	242	CTGCAACTTACTATGTCAACAGGCTAACAGTTCCCGTACACTTTTGGCCAGGGGACCA	301
Db	320	TTGCACTTACTATGTCAACAGGCTAACAGTTCCCTCTCACTTTGGCGGAGGGACCA	379
Qy	302	AGTGGAAATCAACGA	318
Db	380	AGTGGAGATCAACGA	396

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 Job time : 1868.96 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
6520.490 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
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5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	6	ABK89642 DNA encod
2	291.4	91.6	974	6	AAS99473 Anti-huma
3	291	91.5	388	2	AAT73441 Human imm
4	291	91.5	388	2	AAV39239 Functiona
5	291	91.5	388	2	AZ21993 Partial n
6	286.4	90.1	632	7	ABZ22309 S. pneumo
7	285.2	89.7	321	4	AAH47735 Nucleotid
8	283.4	89.1	420	2	AAH73445 Human imm
9	283.4	89.1	420	2	AAV39293 Synthetic
10	283.4	89.1	420	2	AAZ22047 Nucleotid
11	283.4	89.1	3819	2	AAT78825 Kappa lig
12	283.4	89.1	3819	2	AAV39266 Plasmid p
13	283.4	89.1	3819	2	AAZ2020 Nucleotid
14	281.8	88.6	705	9	ADE28412 Human ant
15	280.8	88.3	728	7	ABT31882 Anti-CD40
16	280.4	88.2	321	6	ABA94337 Mab 63 li
17	280.2	88.1	705	9	ADE28428 Human ant
18	278.8	87.7	321	9	ADE28416 Human ant
19	277.2	87.2	321	9	ADE28432 Human ant
20	277	87.1	409	2	AAV39241 Functiona
21	277	87.1	439	2	AAT73443 Human imm
22	275.6	86.7	321	6	AAD46295 Human KDR
23	275.6	86.7	321	7	ABT23330 VEGF bind

24	275.6	86.7	321	9	ADD24425 Human lig
25	275.6	86.7	321	9	ADD80802 Human cLo
26	275.4	86.6	384	2	AAT46133 Monoclonal
27	275.4	86.6	384	2	AAT85844 Monoclonal
28	275.4	86.6	439	2	AZ21995 Partial n
29	274	86.2	321	4	AAF75586 Human ant
30	272.4	85.7	321	4	AAF75588 Human ant
31	270.2	85.0	321	6	ABA94339 Mab 1B7 1
32	269	84.6	684	4	AAH30048 TRO005 ka
33	268.4	84.4	321	5	AAH68654 Human ant
34	268.4	84.4	321	8	ACD45318 Anti-Rh(D
35	267.6	84.2	321	5	AAH26789 Anti-huma
36	267	84.0	322	4	AAF55238 DNA seque
37	267	84.0	322	4	AAF55231 Nucleotid
38	266.8	83.9	321	5	AAH68701 Human ant
39	266.8	83.9	321	8	ACD45365 Anti-Rh(D
40	265.4	83.5	321	6	AAD46301 Human KDR
41	265.4	83.5	321	7	ABT23336 VEGF bind
42	265.4	83.5	321	9	ADD24437 Human lig
43	264.8	83.5	321	9	ADD80814 Human KDR
44	264.8	83.3	333	5	AAH74664 Nucleotid
45	264.8	83.3	426	7	ADA43064 Human ant

## ALIGNMENTS

RESULT 1  
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ID ABK89642 standard; DNA; 318 BP.  
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AC ABK89642;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE DNA encoding human IgE Fab clone 100 light chain.  
XX  
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; PhI p 2;  
KW timothy grass pollen allergen; passive immunotherapy.  
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OS Homo sapiens.  
FH  
FH Key Location/Qualifiers  
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FT /product= "Fab clone 100 heavy chain"  
FT /transl\_except= (pos:193..195, aa:Tyr)  
FT misc\_feature 7..63  
FT /\*tag= b  
FT /\*note= "FR1 region"  
FT misc\_feature 64..96  
FT /\*tag= c  
FT /\*note= "CDR1 region"  
FT misc\_feature 97..141  
FT /\*tag= d  
FT /\*note= "FR2 region"  
FT misc\_feature 142..162  
FT /\*tag= e  
FT /\*note= "CDR2 region"  
FT misc\_feature 163..258  
FT /\*tag= f  
FT /\*note= "FR3 region"  
FT misc\_feature 259..285  
FT /\*tag= g  
FT /\*note= "CDR3 region"  
PN WO200253595-A1.  
PD 11-JUL-2002.  
PF 27-DEC-2001; 2001WO-SE002908.  
XX  
XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX WPI; 2002-583604/62.  
 XX P-PSDB; ABG30450.  
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX Disclosure; Page 35-36; 45pp; English.  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergen patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA  
 CC encoding the human IgG fab, clone 100 light chain protein of the  
 CC invention  
 XX  
 XX Sequence 318 BP; 80 A; 81 C; 81 G; 76 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 318; DB 6; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-93;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCTCAGCAGTCTCCATCTCCGTCGTGTCATCTGTAGGACAGAGTCCACCAACT 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1 GAGCTCAGCAGTCTCCATCTCCGTCGTGTCATCTGTAGGACAGAGTCCACCAACT 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 TGTCGGGGCAGTCAGGCTATTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCCAGGAA 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 TGTCGGGGCAGTCAGGCTATTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCCAGGAA 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 GCCCTAAACTCCTGATCTATTCTGCATCCAGTTGCAAGTGGGTCCCGTCAAGGTTTC 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 GCCCTAAACTCCTGATCTATTCTGCATCCAGTTGCAAGTGGGTCCCGTCAAGGTTTC 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGAT 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 AGCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGCAGCTGAAGAT 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 AAGGTGGAAATCAACGA 318  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 AAGGTGGAAATCAACGA 318  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

## RESULT 2

AAS99473

ID AAS99473 standard; cDNA; 974 BP.

XX

AC AAS99473;

XX

DT 12-MAR-2002 (first entry)

XX

DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.

XX

Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW anti-allergic; antiulcer; neuroprotective; antithyroid; vasotropic;  
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;  
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;  
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;  
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;  
 KW systemic lupus erythematosus; autoimmune disorder; inflammation; ss;  
 KW graft versus host reaction; immune rejection; intestinal immunity;  
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.  
 OS Homo sapiens.  
 XX  
 XX WO200187981-A2.  
 XX 22-NOV-2001.  
 PD 15-MAY-2001; 2001WO-JP004035.  
 XX 18-MAY-2000; 2000JP-00147116.  
 PR 30-MAR-2001; 2001JP-00099508.  
 XX (NITSB ) JAPAN TOBACCO INC.  
 PA  
 XX Tsuji T, Tezuka K, Hori N;  
 PI WPI; 2002-075313/10.  
 XX P-PSDB; AAU74297.  
 DR  
 XX New human monoclonal antibody that binds to activation inducible  
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid  
 PT arthritis, multiple sclerosis and inflammation.  
 XX  
 XX Claim 45; Page 267-270; 300pp; English.

The invention relates to a novel human antibody (I), preferably a human  
 CC monoclonal antibody which binds to an activation inducible lymphocyte  
 CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal  
 CC transduction into a cell mediated by AILIM, for modulating proliferation  
 CC of AILIM-expressing cells, for modulating production of a cytokine from  
 CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity  
 CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of  
 CC AILIM-expressing cells. (I) is useful for treating, preventing or  
 CC prophylaxis of delayed type allergy. (I) is useful for treating and  
 CC preventing various diseases associated with AILIM-mediated costimulatory  
 CC transduction, and for inhibiting the onset and/or advancement of the  
 CC diseases. (I) is useful for suppression, prevention and/or treatment of  
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,  
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,  
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,  
 CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus  
 CC host reaction, graft versus host disease, immune rejection, disorders  
 CC caused by abnormal intestinal immunity, specifically inflammatory  
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,  
 CC nephritis, vasculitis, and pancreatitis. (I) induces no serious  
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse  
 CC antigenicity (HAMA) in a host. AAS99444-AAS99477 represent anti-human  
 CC AILIM monoclonal antibody coding sequences and PCR primers of the  
 CC invention  
 XX  
 XX Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 U; 0 Other;

Query Match 91.6%; Score 291.4; DB 6; Length 974;

Best Local Similarity 95.0%; Pred. No. 4.6e-84;

Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTCCGTCGTGTCATCTGTAGGACAGAGTCCACCAACT 61

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 112 AGATGACCCAGTCTCCATCTCCGTCGTGTCATCTGTAGGACAGAGTCCACCAACT 171

QY 62 GTCGGCGAGTCAGGCTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCCAGGAAAG 121

DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 172 GTCGGCGAGTCAGGCTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCCAGGAAAG 231



CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)  
 CC recombination. The transgenes include a heavy chain transgene comprising  
 CC at least one V, D and J gene segment, and one constant region gene  
 CC segment. The immunoglobulin (Ig) light chain transgene comprises at least  
 CC one V and J gene segment and one constant region gene segment. The gene  
 CC segments are heterologous to the transgenic animal. The antibody can be  
 CC used to prevent efflux of neutrophils from vasculature. It can also be  
 CC used to treat reperfusion injury. CD4 binding antibodies are used to  
 CC reduce undesirable autoimmune reactions, inflammatory responses and  
 CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce  
 CC tissue damage and prolong survival in animal models of acute adult  
 CC respiratory distress syndrome (ARDS) and acid induced lung injury. The  
 CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,  
 CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis  
 XX  
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

Query Match 91.5%; Score 291; DB 2; Length 388;  
 Best Local Similarity 95.2%; Pred. No. 4.3e-84;  
 Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCCTGTCATCTGTAGGACAGAGTCACCACTT 61  
 DB 74 AGATGACCCAGTCTCCATCTTCCGTCCTGTCATCTGTAGGACAGAGTCACCACTT 133  
 QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 121  
 DB 134 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 193  
 QY 122 CCCCTAAACTCCTGATCTATTCATCAGTTTCCAAAGTGGGTCCCGTCAAGTTTCA 181  
 DB 194 CCCCTAAGCTCCTGATCTATGTCATCAGTTTCCAAAGTGGGTCCCGTCAAGTTTCA 253  
 QY 182 GCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAGATT 241  
 DB 254 GCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAGATT 313  
 QY 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
 DB 314 TTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373  
 QY 302 AGGTGGAATCAAC 316  
 DB 374 AGCTGGAGATCAAC 388

RESULT 5  
 AAZ21993  
 ID AAZ21993 standard; DNA; 388 BP.  
 AC AAZ21993;  
 XX  
 DT 24-NOV-1999 (first entry)  
 DE Partial nucleotide sequence for a functional transcript 10C5-kappa.  
 XX  
 KW Transgenic animal; heterologous antibody; hybridoma; B cell;  
 KW transgenic mouse; human heavy chain transgene; digoxin; PCR primer;  
 KW human light chain transgene; immortalized cell; immunoglobulin;  
 KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;  
 KW transplant rejection; blood disorder; coagulation disorder; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9945962-A1.  
 PD 16-SEP-1999.  
 XX  
 PF 12-MAR-1999; 99WO-US005535.  
 XX  
 PR 13-MAR-1998; 98US-00042353.  
 XX

PA (GENP-) GENPHARM INT INC.  
 XX  
 PI Lonberg N, Fishwild DM, Ball WU;  
 XX  
 DR WPI; 1999-551219/46.  
 XX  
 PT Novel transgenic non-human animals used to produce heterologous  
 PT antibodies.  
 XX  
 PS Example 41; Page 305; 484pp; English.  
 XX  
 CC The specification describes transgenic animals that are capable of  
 CC producing a heterologous antibody. The antibodies are isolated from a  
 CC hybridoma, comprising B cells, that is obtained from a transgenic mouse  
 CC having a genome comprising a human heavy chain transgene and a human  
 CC light chain transgene. The B cells are fused to immortalized cells  
 CC suitable for generating a hybridoma, which produces a detectable amount  
 CC of an immunoglobulin that specifically binds digoxin or Shiga-like  
 CC toxin. B cells from transgenic animals can be used to generate hybridomas  
 CC expressing monoclonal high affinity human sequence antibodies. Antibodies  
 CC produced from the transgenic animals of the invention can be used to  
 CC treat human diseases, e.g. autoimmune diseases, cancer, infectious  
 CC disease, transplant rejection, blood disorders such as coagulation  
 CC disorders and other diseases. The present sequence represents a partial  
 CC nucleotide sequence for a functional transcript used in the course of the  
 CC invention  
 XX  
 SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

Query Match 91.5%; Score 291; DB 2; Length 388;  
 Best Local Similarity 95.2%; Pred. No. 4.3e-84;  
 Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCCTGTCATCTGTAGGACAGAGTCACCACTT 61  
 DB 74 AGATGACCCAGTCTCCATCTTCCGTCCTGTCATCTGTAGGACAGAGTCACCACTT 133  
 QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 121  
 DB 134 GTCGGGCGAGTCAGGATATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 193  
 QY 122 CCCCTAAACTCCTGATCTATTCATCAGTTTCCAAAGTGGGTCCCGTCAAGTTTCA 181  
 DB 194 CCCCTAAGCTCCTGATCTATGTCATCAGTTTCCAAAGTGGGTCCCGTCAAGTTTCA 253  
 QY 182 GCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAGATT 241  
 DB 254 GCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAGATT 313  
 QY 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
 DB 314 TTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373  
 QY 302 AGGTGGAATCAAC 316  
 DB 374 AGCTGGAGATCAAC 388

RESULT 6  
 ABZ22309  
 ID ABZ22309 standard; DNA; 632 BP.  
 XX  
 AC ABZ22309;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX  
 DE S. pneumoniae PPS-3 antibody 3H1 light chain DNA sequence SEQ ID NO:4.  
 XX  
 KW Antipneumococcal; antibody; monoclonal antibody; infection; PPS-3;  
 KW Streptococcus pneumoniae; capsular polysaccharide; gene; ds.  
 XX  
 OS Streptococcus pneumoniae.  
 OS Synthetic.





Sat Aug 14 06:09:27 2004

us-10-027-725a-6.rng

ID AAT73445 standard; DNA; 420 BP.  
XX AC AAT73445;  
XX DT 03-DEC-1997 (first entry)  
XX DE Human immunoglobulin light chain variable region partial transcript.  
XX IG; affinity constant; human; antigen; hybridoma; B cell; transgene;  
XX transgenic; mouse; CD4; antibody; autoimmune; inflammatory;  
XX transplanted rejection; ss.  
XX OS Homo sapiens.  
XX FN WO9713852-A1.  
XX PD 17-APR-1997.  
XX PF 10-OCT-1996; 96WO-US016433.  
XX PR 10-OCT-1995; 95US-00544404.  
XX PA (GENP-) GENPHARM INT INC.  
XX PI Lonberg N, Kay RM;  
XX WPI; 1997-235888/21.  
XX Novel anti-CD4 antibody produced by transgenic mice - used in the  
XX treatment of auto-immune disease etc.  
XX Claim 45; Page 272-273; 396pp; English.  
XX A novel composition has been developed which comprises an immunoglobulin  
XX (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M  
XX -1 for binding to a predetermined human antigen. The present sequence  
XX represents a human light chain variable region partial nucleotide  
XX sequence, LC6G5, which encodes an amino acid sequence from a claimed  
XX immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies  
XX may be used in therapeutic and diagnostic applications, especially for  
XX the treatment of human diseases. These antibodies reduce activity of CD4  
XX cells and reduce undesirable autoimmune reactions, inflammatory response  
XX and transplant rejection. Transgenic animals are capable of producing  
XX heterologous antibodies of multiple isotypes by undergoing isotype  
XX switching. These animals produce a first Ig type that is necessary for  
XX antigen-stimulated B-cell maturation and can switch to encode and produce  
XX one or more subsequent heterologous isotypes  
XX  
XX Query Match 89.1%; Score 283.4; DB 2; Length 420;  
XX Best Local Similarity 93.4%; Pred. No. 1.3e-81;  
XX Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTCCGTCGTCTGTCATCTGTAGGACAGAGTCACCATCACTT 61  
Db 80 AGATGACCCAGTCTCCATCTCCGTCGTCTGTCATCTGTAGGACAGAGTCACCATCACTT 139  
QY 62 GTCGGCGAGTCAGGCTATTAGCAGTTGGTATGCTGCTGATCAGCAGAACCCAGGGAAG 121  
Db 140 GTCGGCGAGTCAGGATATTAGCAGCTGTTAGCTGTTATCAGCAGATAAACCCAGGTAAG 199  
QY 122 CCCTTAACCTCCGATCTATTCGATCCAGTTCGAACTGGGGTCCCGTCAAGGTTC 181  
Db 200 CAGCTAAGCTCCGATCTATGCTGTCATCCAGTTTGCAGAGTGGTCCCATCAAGGTTC 259  
QY 182 GCGCAGTGGATCGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 241  
Db 260 GCGGAGTGGATCGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 319  
QY 242 CTGCACTTACTATTGTCAACAGAGCTAACAGTTTCCCGTACACTTTGGCCAGGGACCA 301  
Db 320 TTGCACTTACTATTGTCAACAGAGCTAATAGTTTCCCGTACACTTTTGGTCAGGGACCA 379

QY 302 AGTGGAAATCAACGA 318  
Db 380 AGCTGGAGATCAACGA 396  
RESULT 9  
AAV39293  
ID AAV39293 standard; DNA; 420 BP.  
XX AC AAV39293;  
XX DT 18-DEC-1998 (first entry)  
XX DE Synthetic kappa light chain sequence LC6G5.  
XX Transgenic animal; human heterologous antibody; transgene;  
XX isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;  
XX autoimmune reaction; inflammatory response; transplant rejection;  
XX acid induced lung injury; acute adult respiratory distress syndrome;  
XX ARDS; vasculitis; septic shock; allergic reaction; asthma;  
XX cystic fibrosis; ss.  
XX OS Synthetic.  
XX OS Homo sapiens.  
XX FN WO9824884-A1.  
XX PD 11-JUN-1998.  
XX PF 01-DEC-1997; 97WO-US021803.  
XX PR 02-DEC-1996; 96US-00758417.  
XX (GENP-) GENPHARM INT.  
XX Lonberg N, Kay RM;  
XX WPI; 1998-333306/29.  
XX Hybridoma producing antibody specific for interleukin-8 - used to prevent  
XX efflux of neutrophils from vasculature, and treat reperfusion injury.  
XX  
XX Example 42; Page 324-325; 452pp; English.  
XX The present sequence represents a synthetic kappa light sequence (created  
XX using oligonucleotides AAV39267-78). This synthetic sequence differs from  
XX natural sequences in that strings of repeated oligonucleotides are  
XX interrupted (to facilitate oligonucleotide synthesis and PCR  
XX amplification), optimal translation initiation sites are incorporated and  
XX HindII sites were engineered upstream of the translation initiation  
XX sites. The sequence is used to make plasmid pHC6G5, which is used in the  
XX construction of minigenes for expression of Igkappa anti-CD4 antibodies,  
XX in the transgenic mouse of the invention. The specification describes  
XX transgenic non-human animals, especially a mouse, which are capable of  
XX producing a human heterologous antibodies of multiple isotypes by  
XX undergoing isotype switching. The transgenic animals have human heavy and  
XX light chain transgenes. The transgenes are capable of functionally  
XX rearranging a heterologous diversity (D) gene in a variable-diversity-  
XX junction (V-D-J) recombination. The transgenes include a heavy chain  
XX transgene comprising at least one V, D and J gene segment, and one  
XX constant region gene segment. The immunoglobulin (Ig) light chain  
XX transgene comprises at least one V and J gene segment and one constant  
XX region gene segment. The gene segments are heterologous to the transgenic  
XX animal. The antibody can be used to prevent efflux of neutrophils from  
XX vasculature. It can also be used to treat reperfusion injury. CD4 binding  
XX antibodies are used to reduce undesirable autoimmune reactions.  
XX inflammatory responses and rejection of transplanted organs. The anti-IL-  
XX 8 antibodies can reduce tissue damage and prolong survival in animal  
XX models of acute adult respiratory distress syndrome (ARDS) and acid  
XX induced lung injury. The anti-IL-8 antibodies can also be used for the  
XX treatment of vasculitis, septic shock, allergic reactions (e.g. asthma)  
XX and cystic fibrosis





```
Db      2813 AGCTGGAGATCAAAACGA 2829
RESULT 13
AAZ22020
ID      AAZ22020 standard; DNA; 3819 BP.
XX
AC      AAZ22020;
XX
XX
DT      24-NOV-1999 (first entry)
XX
DE
DE
DE
XX      Nucleotide sequence of plasmid pLC6G5.
XX
XX      Transgenic animal; heterologous antibody; hybridoma; B cell;
KW      transgenic mouse; human heavy chain transgene; digoxin;
KW      human light chain transgene; immortalized cell; immunoglobulin;
KW      Shiga-like toxin; autoimmune disease; cancer; infectious disease;
KW      transplant rejection; blood disorder; coagulation disorder; ss.
XX
XX      Synthetic.
OS
XX
XX      WO9945962-A1.
XX
XX      16-SEP-1999.
XX
XX      12-MAR-1999; 99WO-US005535.
XX
XX      13-MAR-1998; 98US-00042353.
XX
XX      (GENP-) GENPHARM INT INC.
PA
XX
XX      Lonberg N, Fishwild DM, Ball WJ;
PI
XX
XX      WPI; 1999-551219/46.
DR
XX
XX      Novel transgenic non-human animals used to produce heterologous
PT      antibodies.
PT
XX
XX      Example 42; Page 318-320; 484pp; English.
XX
XX      The specification describes transgenic animals that are capable of
CC      producing a heterologous antibody. The antibodies are isolated from a
CC      hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC      having a genome comprising a human heavy chain transgene and a human
CC      light chain transgene. The B cells are fused to immortalized cells
CC      suitable for generating a hybridoma, which produces a detectable amount
CC      of an immunoglobulin that specifically binds digoxin or Shiga-like
CC      toxin. B cells from transgenic animals can be used to generate hybridomas
CC      expressing monoclonal high affinity human sequence antibodies. Antibodies
CC      produced from the transgenic animals of the invention can be used to
CC      treat human diseases, e.g. autoimmune diseases, cancer, infectious
CC      disease, transplant rejection, blood disorders such as coagulation
CC      disorders and other diseases. The present sequence is used in the course
CC      of the invention
XX
XX      Sequence 3819 BP; 947 A; 1015 C; 912 G; 945 T; 0 U; 0 Other;
SQ
Query Match      89.1%; Score 283.4; DB 2; Length 3819;
Best Local Similarity 93.4%; Pred. No. 3.1e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy      2 AGCTCAGCAGTCTCCATCTTCCTGTCTGCTGATCTGTAGGAGACAGATCACCATACTT 61
Db      2513 AGATGACCCAGTCCTCCATCTTCCTGTCTGCTGATCTGTAGGAGACAGATCACCATACTT 2572
Qy      62 GTCGGGGAGTCAGGGGTATTAGCAGTTGGTTAGCTGTATCAGCAGAAACGAGGAAAG 121
Db      2573 GTCGGGGAGTCAGGATATTAGCAGTTGGTTAGCTGTATCAGCATAAACGAGTTAAG 2632
Qy      122 CCCTTAACCTCCTGATCTATTCTGCATCCAGTTTGCAGGTTGGGTCCTCCGTCACAGTTTCA 181
Db      2633 CACCTAAGCTCCTGATCTATGCTGATCCAGTTTGCAGGTTGGTGTCCCATCAAGTTTCA 2692
Qy      182 GCGCAGTGGATCTGGGACAGATTTTCAGTCTCCATCAGCAGCTGCAGCTGAGATT 241
Db      2693 GCGGAAGTGGATCTGGGACAGATTTTCAGTCTCCATCAGCAGCTGCAGCTGAGATT 2752
Qy      242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGGTACACTTTTGGCCAGGGGACCA 301
Db      2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGGTACACTTTTGGTCAGGGAACCA 2812
Qy      302 AGGTGGAATCAAAACGA 318
Db      2813 AGCTGGAGATCAAAACGA 2829
RESULT 14
ADE28412
ID      ADE28412 standard; cDNA; 705 BP.
XX
AC      ADE28412;
XX
XX      29-JAN-2004 (first entry)
DT
DT
XX      Human anti-CD40 antibody 10-8-3 variable region light chain cDNA.
DE
DE
XX      anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW      immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW      bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW      human; variable region light chain; ss; gene; 10-8-3.
XX
XX      Homo sapiens.
OS
XX
XX      WO2003040170-A2.
PN
XX
XX      15-MAY-2003.
PD
XX
XX      08-NOV-2002; 2002WO-US036107.
PF
XX
XX      09-NOV-2001; 2001US-0348980P.
PR
XX
XX      (PFIZ ) PFIZER PROD INC.
PA
XX      (ABGE-) ABGENIX INC.
XX
XX      Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
PI
XX      WPI; 2003-441521/41.
DR
XX      P-PSDB; ADE28413.
DR
XX      New chimeric or human monoclonal antibody or its antigen-binding portion
PT      that specifically binds to and activates human CD40, useful for enhancing
PT      an immune response in a human, or treating cancer, HIV, neutropenia or
PT      viral infections.
XX
XX      Claim 24; SEQ ID NO 19; 177pp; English.
PS
XX
XX      The invention relates to a novel chimeric or human monoclonal antibody or
CC      its antigen-binding portion that specifically binds to and activates
CC      human CD40. The anti-CD40 antibody of the invention demonstrates
CC      cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC      activities and may be useful for treating a hyperproliferative disorder
CC      such as cancer, viral and bacterial infection or genetic, primary or
CC      combined immunodeficiency conditions including neutropenia or HIV
CC      infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC      in a biological sample in vitro or in vivo, as well as during gene
CC      therapy procedures. The current sequence is that of the human anti-CD40
CC      antibody variable region light chain cDNA of the invention.
XX
SQ      Sequence 705 BP; 172 A; 201 C; 179 G; 153 T; 0 U; 0 Other;
Query Match      88.6%; Score 281.8; DB 9; Length 705;
Best Local Similarity 93.1%; Pred. No. 5.3e-81;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy      2 AGCTCAGCAGTCTCCATCTTCCTGTCTGCTGATCTGTAGGAGACAGATCACCATACTT 61
```

Db 68 AGATGACCCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGACACAGAGTCACCATCACTT 127  
QY 62 GTCGGCGGAGTCAGAGTATTAGCACTTGGTTAGCCTGTATCAGCAGAAACCCAGGGAAG 121  
Db 128 GTCGGCGGAGTCAGAGTATTAGCACTTGGTTAGCCTGTATCAGCAGAAACCCAGGGAAG 187  
QY 122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGGTTCA 181  
Db 188 CCCCTAAACTCCTGATCTATTCTGCCTCGGTTTGCAAAAGTGGGTCCCATCAAGTTCA 247  
QY 182 GCGGCGAGTGGATCTCGGACAGATTTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 241  
Db 248 GCGGCGAGTGGATCTCGGACAGATTTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 307  
QY 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 308 TTGCAACTTACTATTGTCAACAGACTGACAGTTTCCCGTCACTTTTCGGCGCGGGGACCA 367  
QY 302 AGGTGGAATCAACGA 318  
Db 368 AGGTGGAGATCAACGA 384

RESULT 15

ABT31882  
ID ABT31882 standard; DNA; 728 BP.  
XX AC ABT31882;  
XX DT 01-MAY-2003 (first entry)  
XX DE Anti-CD40 monoclonal antibody related DNA SEQ ID No 65.  
XX KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;  
KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;  
KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;  
KW immunosuppressor; anti-tumour agent; immunosuppressant; allergy;  
KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;  
XX ds.  
OS Unidentified.  
XX WO200288186-A1.  
XX PD 07-NOV-2002.  
XX PF 26-APR-2002; 2002WO-JF004292.  
XX PR 27-APR-2001; 2001WO-US013672.  
XX PR 11-MAY-2001; 2001JP-00142482.  
XX PR 05-OCT-2001; 2001JP-00310535.  
XX PR 26-OCT-2001; 2001US-00040244.  
XX PA (KIRI ) KIRIN BEER KK.  
XX PI Miyakawa T, Yoshida H, Force WR, Chen X, Takahashi N;  
XX DR WPI: 2003-120463/11.  
XX DR P-PSDB; ABJ36940.

XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,  
PT or functional fragment, is useful in the treatment of e.g. autoimmune  
PT diseases or cancer.  
XX Claim 16; Page 59-60; 94pp; Japanese.  
XX The invention relates to an antibody to human CD40, or its functional  
CC fragment, has at least one of the following properties: acting on  
CC dendritic cells to produce IL-12 in the presence of LPS  
CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic  
CC cells to activate maturity of the dendritic cells with high G28-5  
CC antibody; and activating CD95 expression with high G28-5 antibody against  
CC B cell line. Such antibodies or functional fragments can be used as

CC immunosuppressors, anti-tumour agents, immunosuppressants, and as remedies  
CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors  
CC syndrome. This polynucleotide sequence represents a coding DNA sequence  
CC relating to the anti-CD40 monoclonal antibody of the invention  
XX  
SQ Sequence 728 BP; 183 A; 201 C; 195 G; 149 T; 0 U; 0 Other;

Query Match 88.3%; Score 280.8; DB 7; Length 728;  
Best Local Similarity 93.0%; Pred. No. 1.1e-80;  
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTTCCGTTCTGTCATCTGTAGGACACAGAGTCACCATCACTT 61  
Db 132 AGATGACCCAGTCTCCATCTTCCGTTCTGTCATCTGTAGGACACAGAGTCACCATCACTT 191  
QY 62 GTCGGCGGAGTCAGAGTATTAGCACTTGGTTAGCCTGTATCAGCAGAAACCCAGGGAAG 121  
Db 192 GTCGGCGGAGTCAGAGTATTAGCACTTGGTTAGCCTGTATCAGCAGAAACCCAGGGAAG 251  
QY 122 CCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCCGTCAAGGTTCA 181  
Db 252 CCCCTAAACTCCTGATCTATTCTGCTGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTCA 311  
QY 182 GCGGCGAGTGGATCTCGGACAGATTTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 241  
Db 312 GCGGCGAGTGGATTTGGGACAGATTTTCAGTCTCACCATCAGCAGCCTGAGCCTGAAGATT 371  
QY 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 372 TTGCAACTTACTATTGTCAACAGGCTTAGCAGTTTCCCGTCCGACATTCGGCCAGGGGACCA 431  
QY 302 AGGTGGAATCAACG 317  
Db 432 AGGTGGAGATCAACG 447

Search completed: August 13, 2004, 01:35:55  
Job time : 209.182 secs

	Query Match	100.0.0%;	Score 318;	DB 15;	Length 318;
	Best Local Similarity	100.0.0%;	Pred. No. 3.9e-96;		
	Matches 318;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAGCTCAGCAGTCTCCATCTTCCGGTCTCGCATCTGTAGGACACAGAGTCACCATAACT	60		
DB	1	GAGCTCAGCAGTCTCCATCTTCCGGTCTCGCATCTGTAGGACACAGAGTCACCATAACT	60		
QY	61	TGTGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTTGGTATCAGCAGAAACACAGGGAAA	120		
DB	61	TGTGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTTGGTATCAGCAGAAACACAGGGAAA	120		
QY	121	GCCTCTAACTCCGATCTATTCTGCATCCAGTTTGCAAGTGGGGTCCCGTCAAGGTTTC	180		
DB	121	GCCTCTAACTCCGATCTATTCTGCATCCAGTTTGCAAGTGGGGTCCCGTCAAGGTTTC	180		
QY	181	AGCGGCGAGTGATCTCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT	240		



Db 181 AGCGCAGTGGATCTGGACAGATTTTCAGTCTACCAATCAGCAGCTTGCAGCCTGAGAT 240  
QY 241 TCTGCAACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACC 300  
Db 241 TCTGCAACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACC 300  
QY 301 AAGGTGGAATCAACGA 318  
Db 301 AAGGTGGAATCAACGA 318

RESULT 2  
US-09-859-053-29  
; Sequence 29, Application US/09859053  
; Publication No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 974  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(38)  
; NAME/KEY: CDS  
; LOCATION: (39)...(746)  
; NAME/KEY: 3'UTR  
; LOCATION: (750)...(974)  
; NAME/KEY: sig\_peptide  
; LOCATION: (39)...(104)  
US-09-859-053-29

Query Match 91.6%; Score 291.4; DB 9; Length 974;  
Best Local Similarity 95.0%; Pred. No. 4.6e-87;  
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTCCGTTGCTGCTAGGAGACAGAGTCAACATACTT 61  
Db 112 AGATGACCCAGTCTCCATCTCCGTTGCTGCTAGGAGACAGAGTCAACATACTT 171  
QY 62 GTCGGCGAGTCAGGTATTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGGAAG 121  
Db 172 GTCGGCGAGTCAGGTATTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGGAAG 231  
QY 122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGGTCCCGTCAAGTTCA 181  
Db 232 CCCCTAAACTCTGATCTATTGTCATCCAGTTTGCAGAGTGGGGTCCCGTCAAGTTCA 291  
QY 182 GGGCAGTGGATCGGACAGATTTCACTCTACCATCAGCAGCCTGCAGCCTGAGATT 241  
Db 292 GGGCAGTGGATCGGACAGATTTCACTCTACCATCAGCAGCCTGCAGCCTGAGATT 351  
QY 242 CTCGCACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301  
Db 352 TTCGCACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTGGAGGTTTGGCCAGGGACCA 411  
QY 302 AAGGTGGAATCAACGA 318

Db 412 AGGTGGAATCAACGA 428

RESULT 3  
US-10-309-762-224  
; Sequence 224, Application US/10309762  
; Publication No. US20040018198A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Foltz, Ian  
; APPLICANT: Handa, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
; FILE REFERENCE: ARGENIX.027A  
; CURRENT APPLICATION NUMBER: US/10/309,762  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/337275  
; PRIOR FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 224  
; LENGTH: 322  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-309-762-224

Query Match 90.0%; Score 286.2; DB 16; Length 322;  
Best Local Similarity 94.3%; Pred. No. 1.8e-85;  
Matches 297; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTCCGTTGCTGCTAGGAGACAGAGTCAACATACTT 61  
Db 8 AGATGACCCAGTCTCCATCTCCGTTGCTGCTAGGAGACAGAGTCAACATACTT 67  
QY 62 GTCGGCGAGTCAGGTATTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGGAAG 121  
Db 68 GTCGGCGAGTCAGGTATTAGCAGTTGTTAGCCTGATCAGCAGAAACAGGGAAG 127  
QY 122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGGTCCCGTCAAGTTCA 181  
Db 128 CCCCTAAACTCTGATCTATTGTCATCCAGTTTGCAGAGTGGGGTCCCGTCAAGTTCA 187  
QY 182 GGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGCCTGCAGCCTGAGATT 241  
Db 188 GGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGCCTGCAGCCTGAGATT 247  
QY 242 CTCGCACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301  
Db 248 TTGCAACTTACTATTGCTCAACAGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 307  
QY 302 AGGTGGAATCAAC 316  
Db 308 AAGTGGATATCAAC 322

RESULT 4  
US-10-292-088-23  
; Sequence 23, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: PENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-292-088-23

Query Match      88.6%; Score 281.8; DB 13; Length 705;
Best Local Similarity 93.1%; Pred. No. 6.8e-84;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY  2 AGCTCAGCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 61
Db  68 AGATGCCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 127

QY  62 GTGGGGGAGTCAGGCTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 121
Db  128 GTGGGGGAGTCAGCCTATTAGCAGCTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 187

QY  122 CCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCTCAGGTTCA 181
Db  188 CCCTAAACTCCTGATTTATCTGCCTCCGGTTTGCAGAGTGGGTCCTCAGGTTCA 247

QY  182 GCGCAGTGGATCGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTCAAGATT 241
Db  248 GCGCAGTGGATCGGACAGATTTCATCTCACCATCAGCAGCCTGCAGCCTCAAGATT 307

QY  242 CTGCACTTACTATTGTCAACAGCTTAACAGTTTCCGTTACACTTTTGGCCAGGGACCA 301
Db  308 TTGCACTTACTATTGTCAACAGCTTAACAGTTTCCGTTCACTTTCCGGGGGGGACCA 367

QY  302 AGTGGAATCAAAACGA 318
Db  368 AGTGGAATCAAAACGA 384

RESULT 5
US-09-844-684-15
; Sequence 15, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-15

Query Match      88.3%; Score 280.8; DB 9; Length 728;
Best Local Similarity 93.0%; Pred. No. 1.5e-83;
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY  2 AGCTCAGCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 61
Db  132 AGATGCCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 191

QY  62 GTGGGGGAGTCAGGCTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 121
Db  192 GTGGGGGAGTCAGGCTATTAGCAGCTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 251

QY  122 CCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCTCAGGTTCA 181
Db  252 CCCTAAAGTCTCCTGATCTATCTGATCCAGTTTGCAGAGTGGGTCCTCAGGTTCA 311

QY  182 GCGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTCAAGATT 241
Db  312 GCGCAGTGGATTTGGGACAGATTTCATCTCACCATCAGCAGCCTGCAGCCTCAAGATT 371

QY  242 CTGCACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301
Db  372 TTGCACTTACTATTGTCAACAGGCTTAGCAGTTTCCCTCGGACATTCGGCCCAAGGACCA 431

QY  302 AGTGGAATCAAAACG 317
Db  432 AGTGGAATCAAAACG 447
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QY  182 GCGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTCAAGATT 241
Db  312 GCGCAGTGGATTGGGACAGATTTCACCTCTCACCATCAGCAGCCTGCAGCCTCAAGATT 371

QY  242 CTGCACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301
Db  372 TTGCACTTACTATTGTCAACAGGCTTAGCAGTTTCCCTCGGACATTCGGCCCAAGGACCA 431

QY  302 AGTGGAATCAAAACG 317
Db  432 AGTGGAATCAAAACG 447

RESULT 6
US-10-040-244-15
; Sequence 15, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBO
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 15
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-15

Query Match      88.3%; Score 280.8; DB 15; Length 728;
Best Local Similarity 93.0%; Pred. No. 1.5e-83;
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY  2 AGCTCAGCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 61
Db  132 AGATGCCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 191

QY  62 GTGGGGGAGTCAGGCTATTAGCAGTTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 121
Db  192 GTGGGGGAGTCAGGCTATTAGCAGCTGGTTAGCTGGTATCAGCAGAAACCGAGGAAAG 251

QY  122 CCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCTCAGGTTCA 181
Db  252 CCCTAAAGTCTCCTGATCTATCTGATCCAGTTTGCAGAGTGGGTCCTCAGGTTCA 311

QY  182 GCGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTCAAGATT 241
Db  312 GCGCAGTGGATTTGGGACAGATTTCATCTCACCATCAGCAGCCTGCAGCCTCAAGATT 371

QY  242 CTGCACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301
Db  372 TTGCACTTACTATTGTCAACAGGCTTAGCAGTTTCCCTCGGACATTCGGCCCAAGGACCA 431

QY  302 AGTGGAATCAAAACG 317
Db  432 AGTGGAATCAAAACG 447
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RESULT 7
US-10-693-629-65
; Sequence 65, Application US/10693629
; Publication No. US20040120948A1
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GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; APPLICANT: MIYAYAMA, Toshifumi  
; APPLICANT: YOSHIDA, Hitoshi  
; APPLICANT: FORCE, Walker, R.  
; APPLICANT: CHEN, Xingjie  
; APPLICANT: TAKAHASHI, Nobuaki  
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 021286-0306473  
; CURRENT APPLICATION NUMBER: US/10/693,629  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: PCT/US01/13672  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: JP2001/142482  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: JP2001/310535  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US10/040,244  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-693-629-65

Query Match 88.3%; Score 280.8; DB 17; Length 728;  
Best Local Similarity 93.0%; Pred. No. 1.5e-83;  
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
  
QY 2 AGCTCAGCAGCTCTCCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACCATTAATT 61  
DB 132 AGATGACCCAGCTCTCCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACCATTAATT 191  
  
QY 62 GTCGGCGAGTCAGGATTAAGCAGTTGGTTAGCCTGTCATCTGTAGGAGACAGAGTCAAGGAAAG 121  
DB 192 GTCGGCGAGTCAGGATTAAGCAGTTGGTTAGCCTGTCATCTGTAGGAGACAGAGTCAAGGAAAG 251  
  
QY 122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTCA 181  
DB 252 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTCA 311  
  
QY 182 CGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
DB 312 CGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 371  
  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
DB 372 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 431  
  
QY 302 AGGTGGAATCAAAAG 317  
DB 432 AGGTGGAATCAAAAG 447

RESULT 8  
US-10-324-493-21  
; Sequence 21, Application US/10324493  
; Publication No. US20030124121A1  
; GENERAL INFORMATION:  
; APPLICANT: Plueneke, John  
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 3005-C  
; CURRENT APPLICATION NUMBER: US/10/324,493  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US/09/847,816  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/579,808  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/665,343

PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/785,934  
; PRIOR FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(321)  
US-10-324-493-21

Query Match 88.2%; Score 280.4; DB 15; Length 321;  
Best Local Similarity 93.3%; Pred. No. 1.6e-83;  
Matches 293; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
  
QY 2 AGCTCAGCAGCTCTCCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACCATTAATT 61  
DB 8 AGATGACCCAGCTCTCCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACCATTAATT 67  
  
QY 62 GTCGGCGAGTCAGGATTAAGCAGTTGGTTAGCCTGTCATCTGTAGGAGACAGAGTCAAGGAAAG 121  
DB 68 GTCGGCGAGTCAGGATTAAGCAGTTGGTTAGCCTGTCATCTGTAGGAGACAGAGTCAAGGAAAG 127  
  
QY 122 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTCA 181  
DB 128 CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTGCATCCAGTTTCA 187  
  
QY 182 CGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
DB 188 CGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 247  
  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
DB 248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 307  
  
QY 302 AGGTGGAATCAAA 315  
DB 308 AGGTGGAATCAAA 321

RESULT 9  
US-10-292-088-47  
; Sequence 47, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 705  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-47

Query Match 88.1%; Score 280.2; DB 13; Length 705;  
Best Local Similarity 92.7%; Pred. No. 2.3e-83;  
Matches 294; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
  
QY 2 AGCTCAGCAGCTCTCCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACCATTAATT 61

Db 68 AGATGACCCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGAGTCAACATCACTT 127  
Qy 62 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 121  
Db 128 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 187  
Qy 122 CCCTAAACTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 181  
Db 188 CCCTAAACTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 247  
Qy 182 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 241  
Db 248 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 307  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301  
Db 308 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 367  
Qy 302 AGGTGGAATCAACGA 318  
Db 368 AGGTGGAATCAACGA 384

## RESULT 10

US-10-269-711-28

; Sequence 28, Application US/10269711

; Publication No. US20040071694A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: DeVries, Peter J.

; APPLICANT: Reilly, Edward B.

; APPLICANT: Ostrow, Dave

; APPLICANT: Weiler, James

; APPLICANT: Green, Larry

; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 6989, US.01

; CURRENT APPLICATION NUMBER: US/10/269,711

; CURRENT FILING DATE: 2002-10-14

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 322

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-269-711-28

Query Match 88.0%; Score 279.8; DB 12; Length 322;  
Best Local Similarity 93.0%; Pred. No. 2.5e-83;  
Matches 293; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGAGTCAACATCACTT 61  
Db 8 AGATGACCCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGAGTCTCCATCACTT 67  
Qy 62 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 121  
Db 68 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 127  
Qy 122 CCCTAAACTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 181  
Db 128 CCCTAAAGCTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 187  
Qy 182 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 241  
Db 188 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 247  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301  
Db 248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 307  
Qy 302 AGGTGGAATCAAC 316  
Db 368 AGGTGGAATCAAC 384

Db 308 AAGTGGATATCAAC 322

## RESULT 11

US-10-041-860-85

; Sequence 85, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; FILE REFERENCE: ABGENIX 051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 85

; LENGTH: 322

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-041-860-85

Query Match 88.0%; Score 279.8; DB 15; Length 322;  
Best Local Similarity 93.0%; Pred. No. 2.5e-83;  
Matches 293; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGAGTCAACATCACTT 61  
Db 8 AGATGACCCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGAGTCAACATCACTT 67  
Qy 62 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 121  
Db 68 GTCCGGCGAGTCAGGGTATTAGCAGTTGGTTAGCTGTGTATCAGCAGAAACCCAGGGAAG 127  
Qy 122 CCCTAAACTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 181  
Db 128 CCCTAAAGCTCTGATCTATCTGTCATCCAGTTTGGAAAGTGGGTCCTGTCAGGTTCA 187  
Qy 182 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 241  
Db 188 GCGCAGTGTATCTGGACAGATTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 247  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 301  
Db 248 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGACCA 307  
Qy 302 AGGTGGAATCAAC 316  
Db 308 AGGTGGAATCAAC 322

## RESULT 12

US-10-665-383-63

; Sequence 63, Application US/10665383

; Publication No. US20040141969A1

; GENERAL INFORMATION:

; APPLICANT: Floege, Juergen

; APPLICANT: Gazit, Gadi

; APPLICANT: Keyt, Bruce

; APPLICANT: LaRoche, William

; APPLICANT: Lichtenstein, Henri

; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS

; FILE REFERENCE: ABGENIX.052A

; CURRENT APPLICATION NUMBER: US/10/665,383

; CURRENT FILING DATE: 2003-09-16

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; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 322
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-665-383-63

Query Match      88.0%; Score 279.8; DB 17; Length 322;
Best Local Similarity 93.0%; Pred. No. 2.5e-83;
Matches 293; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCACCATAACTT 61
Db      |||
QY 8 AGATGACCCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCACCATCACTT 67
Db      |||
QY 62 GTCGGCGAGTCAGGATATAGAGTTGGTATAGCCTGTAGCTGTATCAGCAGAAACAGGGAAG 121
Db      |||
QY 69 GTCGGCGAGTCAGGATATAGAGTTGGTATAGCCTGTAGCTGTATCAGCAGAAACAGGGAAG 127
Db      |||
QY 122 CCCCTAAACTCTCTGATCTATCTGCATCTCTGCATCTCTAGGAGACAGATCACCATAACTT 181
Db      |||
QY 128 CCCCTAAAGTCTCTGATCTATCTGCATCTCTGCATCTCTAGGAGACAGATCACCATAACTT 187
Db      |||
QY 182 GCGGAGTGGATCTCGGACAGATTTTCACTCTCACCATCAGCAGCTTGCAGCTTGAAGATT 241
Db      |||
QY 188 GCGGAGTGGATCTCGGACAGATTTTCACTCTCACCATCAGCAGCTTGCAGCTTGAAGATT 247
Db      |||
QY 242 CTGCAACTTACTTATTTGTCAGAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db      |||
QY 248 TTGCACTTACTTATTTGTCAGAGCTGACAGTTTCCCGTCACTTTTCGGCGGGGACCA 307
Db      |||
QY 302 AGGTGGAATCAAA 315
Db      |||
QY 308 AGGTGGAATCAAA 321
Db      |||

RESULT 14
US-10-269-711-16
; Sequence 15, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: DeVries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989 US 01
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-16

Query Match      87.5%; Score 278.2; DB 12; Length 322;
Best Local Similarity 92.7%; Pred. No. 8.5e-83;
Matches 292; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCACCATAACTT 61
Db      |||
QY 8 AGATGACCCAAATCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCTCCATCACTT 67
Db      |||
QY 62 GTCGGCGAGTCAGGATATAGCAGTTGGTATAGCCTGTATCAGCAGAAACAGGGAAG 121
Db      |||
QY 68 GTCGGCGAGTCAGGATATAGCAGTTGGTATAGCCTGTATCAGCAGAAACAGGGAAG 127
Db      |||
QY 122 CCCCTAAACTCTCTGATCTATCTGCATCTTCAGTGGGTCCCGTCAAGTTCA 181
Db      |||
QY 128 CCCCTAGCTCTTAATCTATCTGCTGATCCAGTTTGCACGTGGGTCCCATCAAGTTCA 187
Db      |||
QY 182 GCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTTGCAGCTTGAAGATT 241
Db      |||
QY 188 GCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTTGCAGCTTGAAGATT 247
Db      |||
QY 242 CTGCAACTTACTTATTTGTCAGAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db      |||
QY 248 TTGCACTTACTTATTTGTCAGAGCTGACAGTTTCCCGTCACTTTTCGGCGGGGACCA 307
Db      |||
QY 302 AGGTGGAATCAAA 316
Db      |||
QY 308 AAGTGGATATCAAA 322
Db      |||

RESULT 15
US-10-292-088-19
; Sequence 19, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-19

Query Match      87.7%; Score 278.8; DB 13; Length 321;
Best Local Similarity 93.0%; Pred. No. 5.4e-83;
Matches 292; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCACCATAACTT 61
Db      |||
QY 8 AGATGACCCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGATCACCATCACTT 67
Db      |||
QY 62 GTCGGCGAGTCAGGATATAGCAGTTGGTATAGCCTGTATCAGCAGAAACAGGGAAG 121
Db      |||
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-10-027-725A-6  
Perfect score: 318

Sequence: 1 gagctcagcagctccatc.....ccaaaggtggaatacaacga 318

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	91.5	388	3	US-09-042-353-358
2	291	91.5	388	4	US-08-758-417A-206
3	283.4	89.1	420	3	US-09-042-353-420
4	283.4	89.1	420	4	US-08-758-417A-220
5	283.4	89.1	3819	3	US-09-042-353-393
6	283.4	89.1	3819	4	US-08-758-417A-243
7	277	87.1	439	3	US-09-042-353-360
8	277	87.1	439	4	US-08-758-417A-208
9	275.4	86.6	384	1	US-08-259-372A-13
10	275.4	86.6	384	1	US-08-468-671-13
11	268.4	84.4	321	3	US-09-240-274-109
12	268.8	83.9	321	3	US-09-240-274-199
13	263.6	82.9	321	3	US-09-240-274-98
14	263.6	82.9	321	3	US-09-240-274-102
15	263.6	82.9	321	3	US-09-240-274-218
16	263.6	82.9	321	3	US-09-240-274-221
17	263.6	82.9	321	3	US-09-240-274-222
18	262	82.4	321	3	US-09-240-274-215
19	262	82.4	321	3	US-09-240-274-217
20	260.4	81.9	321	3	US-09-240-274-113
21	259.4	81.6	324	2	US-08-378-939-31
22	259.4	81.6	324	2	US-08-378-939-33
23	259.4	81.6	714	4	US-09-472-087-62
24	258.8	81.4	321	3	US-08-240-274-107
25	257.8	81.1	390	2	US-08-646-367-2
26	257.2	80.9	321	3	US-09-240-274-105
27	257.2	80.9	321	3	US-09-240-274-216

## ALIGNMENTS

RESULT 1  
US-09-042-353-358  
; Sequence 358, Application US/09042353  
; Patent No. 6255458  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 421  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,353  
; FILING DATE: 13-MAR-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/096,762  
; FILING DATE: 22-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/155,301  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,739  
; FILING DATE: 03-DEC-1993

Sequence 206, App  
Sequence 23, Appl  
Sequence 104, App  
Sequence 201, App  
Sequence 211, App  
Sequence 101, App  
Sequence 112, App  
Sequence 17, Appl  
Sequence 207, App  
Sequence 15, Appl  
Sequence 106, App  
Sequence 224, App  
Sequence 205, App  
Sequence 110, App  
Sequence 48, Appl  
Sequence 36, Appl  
Sequence 36, Appl

28 257 80.8 324 3 US-09-240-274-206  
29 256.2 80.6 324 2 US-08-378-939-23  
30 255.6 80.4 321 3 US-09-240-274-104  
31 255.6 80.4 321 3 US-09-240-274-201  
32 255.6 80.4 321 3 US-09-240-274-211  
33 255.4 80.3 324 3 US-09-240-274-101  
34 255.4 80.3 324 3 US-09-240-274-112  
35 255.4 80.3 324 3 US-09-240-274-210  
36 254.6 80.1 324 2 US-08-378-939-17  
37 254 79.9 321 3 US-09-240-274-207  
38 253 79.6 324 2 US-08-378-939-15  
39 252.4 79.4 321 3 US-09-240-274-106  
40 252.2 79.3 324 3 US-09-240-274-224  
41 250.8 78.9 321 3 US-09-240-274-205  
42 250.6 78.8 324 3 US-09-240-274-110  
43 250.2 78.7 417 4 US-09-472-087-48  
44 250 78.6 321 3 US-08-599-226-36  
45 250 78.6 321 3 US-09-125-098-36





Db 194 CCGCTAAGCTCTGATCTATGCTGATCCAGTTTCCTCAAGTGGGTCCCATCAGGTTCA 253  
Qy 182 GCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTCTGAGCTGAAGATT 241  
Db 254 GCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTCTGAGCTGAAGATT 313  
Qy 242 CTGCAACTTACTATTGTCTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 314 TTGCACTTACTATTGTCTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 373  
Qy 302 AGGTGGAATCAAC 316  
Db 374 AGCTGGAGATCAAC 388

## RESULT 3

US-09-042-353-420  
; Sequence 420, Application US/09042353  
; Patent No. 6255458  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 421  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,353  
; FILING DATE: 13-MAR-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/096,762  
; FILING DATE: 22-JUL-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/155,301  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,739  
; FILING DATE: 03-DEC-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,699  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/209,741  
; FILING DATE: 09-MAR-1994  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/352,322  
; FILING DATE: 07-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/544,404  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/728,463  
; FILING DATE: 10-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US96/16433  
; FILING DATE: 10-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/758,417  
; FILING DATE: 02-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/21803  
; FILING DATE: 01-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 014643-009040US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 420:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 420 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-042-353-420

Query Match 89.1%; Score 283.4; DB 3; Length 420;  
Best Local Similarity 93.4%; Pred. No. 4e-87;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCGGTGTCTGATCTGTAGGAGACAGAGTCAACCAACTT 61  
Db 80 AGATGACCCAGTCTCCATCTTCGGTGTCTGATCTGTAGGAGACAGAGTCAACCAACTT 139  
Qy 62 GTCGGGGAGTCTGGGATTTAGCAGTTGGTGGTGGTATCAGCAGAAACCGGAAAG 121  
Db 140 GTCGGGGAGTCTGGGATTTAGCAGTTGGTGGTGGTATCAGCAGAAACCGGAAAG 199  
Qy 122 CCCTAAACTCTCTGATCTATCTGATCCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAGTTTCA 181  
Db 200 CACCTAAGCTCTGATCTATCTGATCCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAGTTTCA 259  
Qy 182 GCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGACGCTGAAGATT 241  
Db 260 GCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCTGACGCTGAAGATT 319  
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 320 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 379  
Qy 302 AGGTGGAATCAACGA 318  
Db 380 AGCTGGAGATCAACGA 396

## RESULT 4

US-08-758-417A-220  
; Sequence 220, Application US/08758417A  
; Patent No. 6300129  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 417  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-Dec-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 28-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 220:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 420 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 220:

US-08-758-417A-220  
Query Match 89.1%; Score 283.4; DB 4; Length 420;  
Best Local Similarity 93.4%; Pred. No. 4e-87;  
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 2 AGCTACGAGTCTCCATCTTCGGTCTCGATCTGTAGGACAGAGTCACCATACCTT 61  
DB 80 AGATGACCCAGTCTCCATCTTCGGTCTCGATCTGTAGGACAGAGTCACCATACCTT 139  
QY 62 GTCGGGCGAGTCAGGATATTAGCAGTTGTTAGCCTGTTATCAGCAGAAACCCAGGAAAG 121  
DB 140 GTCGGGCGAGTCAGATATTAGCAGTGTGTAGCCTGTTATCAGCATAACCCAGGTAAG 199  
QY 122 CCCCTAAATCTCTGATCTATTCTGATCCAGTTTGCAAGTGGGTCCTGTCAGGTTCA 181  
DB 200 CACCTAAGCTCTCTGATCTATTGTGATCCAGTTTGCAAGTGGTGTCCCATCAAGGTTCA 259  
QY 182 GCGGCGAGTGGACTGGGACAGATTTTCAGTCTCACCATCAGCCCTGCAGCCTGAAGATT 241  
DB 260 GCGGAAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCCCTGCAGCCTGAAGATT 319

QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTCCTCGTACACTTTTCCGTCAGGAGCA 301  
DB 320 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCGTCACACTTTTGGTCAGGAGCA 379  
QY 302 AGGTGGAAATCAACGA 318  
DB 380 AGCTGGAGATCAACGA 396  
RESULT 5  
US-09-042-353-393  
; Sequence 393, Application US/09042353  
; Patent No. 6255458  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 421  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,353  
; FILING DATE: 13-MAR-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/096,762  
; FILING DATE: 22-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/155,301  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,739  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,699  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/209,741  
; FILING DATE: 09-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/352,322  
; FILING DATE: 07-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/544,404  
; FILING DATE: 10-OCT-1995  
; APPLICATION NUMBER: US 08/728,463

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; FILING DATE: 10-OCT-1996
; PRIORITY APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-042-353-393

Query Match      89.1%; Score 283.4; DB 3; Length 3819;
Best Local Similarity 93.4%; Pred. No. 1.1e-86;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCGAGTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCAACCAACTT 61
DB 2513 AGATGACCCAGTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCAACCAACTT 2572

QY 62 GTCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGTGATCAGAGAAACAGGGAAG 121
DB 2573 GTCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGTGATCAGAGAAACAGGGAAG 2632

QY 122 CCCCTAAACTCTCTGATCTATTTCTGCATCCAGTTTGCAGGTCCTCCGTCAGGTTCA 181
DB 2633 CACCTAAGCTCTCTGATCTATGCTGCATCCAGTTTGCAGGTCCTCCGTCAGGTTCA 2692

QY 182 GCGGCGAGTCAGGATTTAGCAGTTTTCAGTCTCAGCTCAGAGCTGCGAGCTGAAGATT 241
DB 2693 GCGGCGAGTCAGGATTTAGCAGTTTTCAGTCTCAGCTCAGAGCTGCGAGCTGAAGATT 2752

QY 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTCACACTTTTGGCAGGGAACCA 301
DB 2753 TTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTCACACTTTTGGCAGGGAACCA 2812

QY 302 AGGTGGAATCAAAACGA 318
DB 2813 AGCTGGAGATCAAAACGA 2829

RESULT 6
US-08-758-417A-243
; Sequence 243, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 243:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243

Query Match      89.1%; Score 283.4; DB 4; Length 3819;
Best Local Similarity 93.4%; Pred. No. 1.1e-86;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCGAGTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCAACCAACTT 61
DB 2513 AGATGACCCAGTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCAACCAACTT 2572

QY 62 GTCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGTGATCAGAGAAACAGGGAAG 121
DB 2573 GTCGGGCGAGTCAGGATTTAGCAGTTGGTTAGCTGTGATCAGAGAAACAGGGAAG 2632

QY 122 CCCCTAAACTCTCTGATCTATTTCTGCATCCAGTTTGCAGGTCCTCCGTCAGGTTCA 181
DB 2633 CACCTAAGCTCTCTGATCTATGCTGCATCCAGTTTGCAGGTCCTCCGTCAGGTTCA 2692

QY 182 GCGGCGAGTCAGGATTTAGCAGTTTTCAGTCTCAGCTCAGAGCTGCGAGCTGAAGATT 241
DB 2693 GCGGCGAGTCAGGATTTAGCAGTTTTCAGTCTCAGCTCAGAGCTGCGAGCTGAAGATT 2752

QY 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTCACACTTTTGGCAGGGAACCA 301
DB 2753 TTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTCACACTTTTGGCAGGGAACCA 2812

QY 302 AGGTGGAATCAAAACGA 318
DB 2813 AGCTGGAGATCAAAACGA 2829
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; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-08-758-417A-208

Query Match      87.1%; Score 277; DB 4; Length 439;
Best Local Similarity 92.1%; Pred. No. 6.2e-85;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY      2 AGCTCAGCAGTCTCCATCTCCGTCCTGCATCTGTAGGACAGAGTCAACATACTT 61
Db      74 AGATGCCAGTCTCCATCTCTACTGTCATCTGTAGGACAGAGTCAACATACTT 133
QY      62 GTCCGGCAGTCAGGGTATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 121
Db      134 GTCCGGCAGTCAGGGTATTAGCAGTGTGTAGCTGTATCAGCAGAAACCCAGGAAAG 193
QY      122 CCCTAAACTCCGTATCTATCTGCATCCAGTTTGCAGAGTGGGTCCTCGTCAAGTTCA 181
Db      194 CCCTAAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCTCGTCAAGTTCA 253
QY      182 GCAGCAGTGGATCTGGACAGATTTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 241
Db      254 GCAGCAGTGGATCTGGACAGATTTTCACTCTCACCATCAGCAGCTCAGCCTGAAGATT 313
QY      242 CTGCAACTTACTATGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301
Db      314 TTGCAACTTATTACTGCCAAGATGATGATGATTACCCGTACACTTTTGGCCAGGGGACCA 373
QY      302 AGTGGAAATCAACGA 318
Db      374 AGCTGGAGATCAACGA 390

RESULT 9
US-08-259-372A-13
; Sequence 13, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
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; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Hybridoma
; CELL LINE: ZM1-2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..384
; US-08-259-372A-13

Query Match      86.6%; Score 275.4; DB 1; Length 384;
Best Local Similarity 91.8%; Pred. No. 2.1e-84;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY      2 AGCTCAGCAGTCTCCATCTCCGTCCTGCATCTGTAGGACAGAGTCAACATACTT 61
Db      68 AGATGCCAGTCTCCATCTCTCGTCATCTGTGGGAGACAGAGTCAACGTCACCT 127
QY      62 GTCCGGCAGTCAGGGTATTAGCAGTTGGTTAGCTGTATCAGCAGAAACCCAGGAAAG 121
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Db 128 GTCGGGAGTCAGGATTAGCAGTTGGTTAGCTGTGATCAGCAGAAACCCAGGAAAG 187  
QY 122 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCRAAGTGGGTCCCGTCAAGTTTCA 181  
Db 188 CCCCTAACTCTGATCATCTGTCATCCAGTTTGCRAAGTGGGTCCCGTCAAGTTTCA 247  
QY 182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
Db 248 TCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 307  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 308 TTGCAACCTACTATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTTCCGCGAGGGACCA 367  
QY 302 AGGTGGAATCAACGA 318  
Db 368 AGGTGGACTTCAACGA 384

RESULT 10

US-08-468-671-13  
; Sequence 13, Application US/08468671  
; Patent No. 5648077  
; GENERAL INFORMATION:  
; APPLICANT: Ostberg, Lars G.  
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,671  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/259,372  
; FILING DATE: 14-JUN-1994  
; APPLICATION NUMBER: US 07/871,426  
; FILING DATE: 21-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/676,036  
; FILING DATE: 27-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/538,796  
; FILING DATE: 15-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/192,754  
; FILING DATE: 11-MAY-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/925,196  
; FILING DATE: 31-OCT-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/904,517  
; FILING DATE: 05-SEP-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-50-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 384 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Hybridoma  
CELL LINE: ZMI-2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..384  
US-08-468-671-13  
Query Match 86.6%; Score 275.4; DB 1; Length 384;  
Best Local Similarity 91.8%; Pred. No. 2.1e-84;  
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 2 AGCTCAGCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATTAATT 61  
Db 68 AGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTGGGAGACAGAGTCACCGTCACTT 127  
QY 62 GTCGGGAGTCAGGATTATTAGCAGTTGGTTAGCTGTGATCAGCAGAAACCCAGGAAAG 121  
Db 128 GTCGGGAGTCAGGATTATTAGCAGTTGGTTAGCTGTGATCAGCAGAAACCCAGGAAAG 187  
QY 122 CCCCTAACTCTGATCTATTCTGCATCCAGTTTGCRAAGTGGGTCCCGTCAAGTTTCA 181  
Db 188 CCCCTAACTCTGATCATCTGTCATCCAGTTTGCRAAGTGGGTCCCGTCAAGTTTCA 247  
QY 182 GCGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 241  
Db 248 TCGGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGATT 307  
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACCA 301  
Db 308 TTGCAACCTACTATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTTCCGCGAGGGACCA 367  
QY 302 AGGTGGAATCAACGA 318  
Db 368 AGGTGGACTTCAACGA 384

RESULT 11

US-09-240-274-109  
; Sequence 109, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 109  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain I09  
US-09-240-274-109

Query Match 84.4%; Score 268.4; DB 3; Length 321;  
Best Local Similarity 90.3%; Pred. No. 4.7e-82;  
Matches 287; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 60  
DB |||||  
4 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 63  
DB |||||  
QY 61 TGTGGGCGAGTCAGGCTATTAGCAGTCTGGTTAGCCTGCTATCAGCAGAAACACAGGAAA 120  
DB |||||  
64 TGGCGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACACAGGAAA 123  
DB |||||  
QY 121 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 180  
DB |||||  
124 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 183  
DB |||||  
QY 181 AGCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 240  
DB |||||  
184 AGTGGCAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 243  
DB |||||  
QY 241 TCTCAACTTACTATTGTCAACAGCTAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
DB |||||  
244 TTTGCACTTATTACTGTCAACAGCTTAATAGTTACCGGTACACTTTTGGCCAGGGGACC 303  
DB |||||  
QY 301 AAGCTGGAATCAACGA 318  
DB |||||  
304 AAGCTGGAGATCAACGA 321  
DB |||||

## RESULT 12

US-09-240-274-199

; Sequence 199, Application US/09240274

; Patent No. 6255455

; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; FILE REFERENCE: 09596-4202

; CURRENT APPLICATION NUMBER: US/09/240,274

; EARLIER FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: 60/081,380

; EARLIER FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/028,550

; EARLIER FILING DATE: 1996-10-11

; NUMBER OF SEQ ID NOS: 224

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 199

; LENGTH: 321

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: anti-Rh(D) antibody clone SH13

US-09-240-274-199

Query Match 83.9%; Score 266.8; DB 3; Length 321;  
Best Local Similarity 89.9%; Pred. No. 1.6e-81;  
Matches 286; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 60  
DB |||||  
4 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 63  
DB |||||  
QY 61 TGTGGGCGAGTCAGGCTATTAGCAGTCTGGTTAGCCTGCTATCAGCAGAAACACAGGAAA 120  
DB |||||  
64 TGGCGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACACAGGAAA 123  
DB |||||  
QY 121 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 180  
DB |||||  
124 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 183  
DB |||||  
QY 181 AGCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 240  
DB |||||  
184 AGTGGCAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 243  
DB |||||  
QY 241 TCTCAACTTACTATTGTCAACAGCTTAATAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
DB |||||

DB 244 TTTGCACTTACTACTGTCAACAGATTACAGTACAGTACCCCTACACTTTTGGCCAGGGGACC 303  
QY 301 AAGCTGGAATCAACGA 318  
DB |||||  
304 AAGCTGGAGATCAACGA 321  
DB |||||

## RESULT 13

US-09-240-274-96

; Sequence 98, Application US/09240274

; Patent No. 6255455

; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; FILE REFERENCE: 09596-4202

; CURRENT APPLICATION NUMBER: US/09/240,274

; EARLIER FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: 60/081,380

; EARLIER FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/028,550

; EARLIER FILING DATE: 1996-10-11

; NUMBER OF SEQ ID NOS: 224

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 98

; LENGTH: 321

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: anti-Rh(D) chain F01

US-09-240-274-96

Query Match 82.9%; Score 263.6; DB 3; Length 321;  
Best Local Similarity 89.3%; Pred. No. 2e-80;  
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 60  
DB |||||  
4 GAGCTCAGCAGCTCTCCATCTTCGTCGTGATCTGTAGGAGACAGAGTCAACATAACT 63  
DB |||||  
QY 61 TGTGGGCGAGTCAGGCTATTAGCAGTCTGGTTAGCCTGCTATCAGCAGAAACACAGGAAA 120  
DB |||||  
64 TGGCGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACACAGGAAA 123  
DB |||||  
QY 121 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 180  
DB |||||  
124 GCCCTAACTCTGATCTATTCGATCTCCAGTTTGAAAGTGGGTCCTCCTCAAGGTTTC 183  
DB |||||  
QY 181 AGCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 240  
DB |||||  
184 AGCGGAGTGGATCTGGGACAGATTCAGTCTCACCATCAGCAGCCTGAGCTGAAGAT 243  
DB |||||  
QY 241 TCTGCAACTTACTATTGTCAACAGCTTAATAGTTTCCCGTACACTTTTGGCCAGGGGACC 300  
DB |||||  
244 TCTGCAACTTACTATTGTCTACAGCATTAATAGTTTCCCGTGGACGTTTCGGCCCAAGGGACC 303  
DB |||||  
QY 301 AAGCTGGAATCAACGA 318  
DB |||||  
304 AAGCTGGAATCAACGA 321  
DB |||||

## RESULT 14

US-09-240-274-102

; Sequence 102, Application US/09240274

; Patent No. 6255455

; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; FILE REFERENCE: 09596-4202

; CURRENT APPLICATION NUMBER: US/09/240,274

; EARLIER FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: 60/081,380

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; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match      82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 2e-80; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      1  GAGCTCAGCGAGTCTCCATCTTCCTGTCGATCTGTAGGAGACAGAGTCACCGTCACT 63
Db
QY      61  TGTGGGGGAGTCAGGGTATTAGCAGTTGGTTAGCCCTGGTATCAGCAGAAACCCAGGGAAA 120
Db
QY      64  TGCAGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAACCCAGGGAAA 123
Db
QY      121  GCCCTAAACTCCTGATCTATTCTGCATCCAGTTTGCAGTTTGCAGTTTGGGGTCCCGTCAAGGTTT 180
Db
QY      124  GCCCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAGTTTGCAGTTTGGGGTCCCGTCAAGGTTT 183
Db
QY      181  AGCGGCGAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCTGAAGAT 240
Db
QY      184  AGTGGCAGTGGATCTGGGACAGATTTCAGTCTCACCATCAGCAGTCTGCAACCTGAAGAT 243
QY      241  TCTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
Db
QY      244  TTTGCAACTTACTACTGTCAACAGGTTACAGTACCCCGTGGACGTTTCGGCCCAAGGGACC 303
QY      301  AAGGTGGAATCAAAACGA 318
Db
QY      304  AAGGTGGAATCAAAACGA 321

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Search completed: August 13, 2004, 07:18:10  
Job time : 44.9697 secs

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RESULT 15
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

Query Match      82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 2e-80; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      1  GAGCTCAGCGAGTCTCCATCTTCCTGTCGATCTGTAGGAGACAGAGTCACCGTCACT 60

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 10.0182 Seconds  
(without alignments)  
1094.593 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGPGLVKPAQTLSLCAV.....RLDGVTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479.5	78.7	116	2 S37456	Ig mu chain - huma
2	476.5	78.2	135	2 S78051	Ig heavy chain pre
3	475.5	78.1	128	2 S31514	Ig heavy chain - h
4	465	76.4	122	2 S69912	Ig V-D-J region (N
5	464.5	76.3	147	2 S13519	Ig heavy chain V r
6	460	75.5	130	2 S30534	Ig heavy chain V r
7	458.5	75.3	140	2 I37782	Ig variable region
8	453	74.4	99	2 S26801	Ig heavy chain V r
9	452.5	74.3	146	2 S09710	Ig heavy chain V r
10	451.5	74.1	121	2 S44113	Ig heavy chain V r
11	451.5	74.1	130	2 S31690	Ig heavy chain V r
12	450.5	74.0	127	2 S19668	Ig heavy chain V r
13	450.5	74.0	146	2 S09711	Ig heavy chain V r
14	449.5	73.8	155	2 S31511	Ig heavy chain - h
15	446.5	73.3	155	2 S31512	Ig heavy chain - h
16	444	72.9	137	2 S31676	Ig heavy chain V r
17	440	72.2	139	2 S31586	Ig heavy chain pre
18	439	72.1	145	2 S78055	Ig heavy chain V r
19	436	71.6	99	2 S26803	Ig heavy chain pre
20	435.5	71.5	123	2 S30530	Ig heavy chain V r
21	434	71.3	129	2 S44114	Ig heavy chain V r
22	433.5	71.2	117	2 E34964	Ig heavy chain pre
23	432.5	71.0	109	2 PH1673	Ig heavy chain V r
24	431	70.8	99	2 S26802	Ig heavy chain V r
25	430	70.6	97	2 PL0118	Ig heavy chain V-I
26	430	70.6	99	2 S26899	Ig heavy chain V r
27	427	70.1	110	2 S44110	Ig heavy chain V-D
28	426	70.0	139	2 A41287	Ig heavy chain pre
29	425.5	69.9	121	2 C55257	Ig gamma heavy Cha

ALIGNMENTS

RESULT 1

S37456

Ig mu chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S37456

R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.

submitted to the EMBL Data Library, September 1993

A:Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from

A:Reference number: S37453

A:Accession: S37456

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-116 <MCI>

A:Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 479.5; DB 2; Length 116;

Best Local Similarity 76.1%; Pred. No. 4.6e-38;

Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

Qy 6 GLVKPAQTLSLSCAVSGGSISSGGYWSWIRQHPGKLEWIGYIHSGNTYNPSLKSRI 65

Db 1 GLVKPSQTLSLTCTVSGSISGGYWSWIRQHPGKLEWIGYIHSGNTYNPSLKSRI 60

Qy 66 AMSVDTSENKFSRLNSVTAADTAIVYCARLGDYT-----LDIWGQGLTVTVSS 114

Db 61 TISVDTSKNQFSKLKLSVTAADTAIVYCAR-GGYSYGYVYVMDVWGKGTITVTVSS 116

RESULT 2

S78051

Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999

C:Accession: S78051; S23716

R:Harindranath, N.

submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78051

A:Molecule type: mRNA

A:Residues: 1-135 <HAR>

A:Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g9930117

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin;

Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and J

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23716

A:Molecule type: mRNA

```

A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match      78.2%; Score 476.5; DB 2; Length 135;
Best Local Similarity 76.3%; Pred. No. 1e-37;
Matches 90; Conservative 13; Mismatches 10; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYINPNSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 ESGPGLVKPSETLSLTCVSGGSIIRSGHYWIRQHPGKLEWIGSIYIYHSGNTYINPNSL 77
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARL--DGYTL---DINGQGTFLVTSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 KSRVTSISVDTSKNQFSLKLSVTAADTAVYYCARLGPDDYTLDGMVWGQGTFLVTSS 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CRA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match      78.1%; Score 475.5; DB 2; Length 128;
Best Local Similarity 76.7%; Pred. No. 1.2e-37;
Matches 89; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYINPNSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 13 ESGPGLVRPSQTLSTLCTVSGGSIIRSGGYWIRQHPGMALEWIAHYIFSGSTYINPPL 72
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLD--GYTLDIWGQGTFLVTSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 73 KSRVTSISVDTSENKFSRLNSVTPADTAVYYCARIGYGFDPWGQGTFLVTSS 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S69912
Ig V-D-J region (ND) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: S69909, MUID:94335315; PMID:8057663
A;Accession: S69912
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: EMBL:Z33398; NID:g871347; PIDN:CRA83849.1; PID:g9887460
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match      76.4%; Score 465; DB 2; Length 122;

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Best Local Similarity 75.2%; Pred. No. 1.1e-36;
Matches 88; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYINPNSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPQSQTLSLTCVSGGSIIRSGHFWIRQHPGKLEWIGNIYFSGSYINPNSL 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCAR---LDGYTLDIWGQGTFLVTSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTSISVDTSKNQFSLKLSVTAADTAVYFCARGFFFRGTGLDTWGQGTFLVRLSS 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CRA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match      76.3%; Score 464.5; DB 2; Length 147;
Best Local Similarity 75.9%; Pred. No. 1.5e-36;
Matches 88; Conservative 11; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYINPNSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 32 ESGPGLVKPSETLSLTCVSGGSIIRSSSYWIRQHPGKLEWIGSIYIYHSGNTYINPNSL 91
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCAR---LDGYTLDIWGQGTFLVTSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 92 KSRVTSISVDTSKNQFSLKLSVTAADTAVYCARPLWFGELFDYWGQGTFLVTSS 147
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match      75.5%; Score 460; DB 2; Length 130;
Best Local Similarity 72.8%; Pred. No. 3.5e-36;
Matches 91; Conservative 10; Mismatches 12; Indels 12; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYINPNSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGSYWIRQHPGKLEWIGRIYTSGSTYINPNSL 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDG-----YT-----LDIWGGTFL 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTSISVDTSKNQFSLKLSVTAADTAVYCARDKGFWSGYIYTRNSRAAFDIWGQGT 125
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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QY      110 VTVSS 114
      |||||
Db      126 VTVSS 130

RESULT 7
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: I37782; S25476
R:Demaison, C.; Chastagner, P.; Therez, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A36876; MUID:94119917; PMID:8290556
A:Accession: I37782
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:45-128/Domain: immunoglobulin homology <IMM>

Query Match      75.3%; Score 458.5; DB 2; Length 140;
Best Local Similarity 75.4%; Pred. No. 5.3e-36;
Matches 89; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

QY      2  ESGPGLVKPAQTLSLSCAVSGGSGIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db      25  ESGPGLVKPSETLSLTCTVSGGSISS--YVWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 82

QY      62  KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG-----GYTLDTWGQGLTVTVSS 114
Db      83  KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARHNSSSWYGRYFDYWGQGLTVTVSS 140

RESULT 8
S26801
Ig heavy chain V region (DP-65) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C:Accession: S26801; S26900
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26801
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WEN>
A:Cross-references: EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID:g335372
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26900
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <TOM>
A:Cross-references: EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID:g32949
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match      74.4%; Score 453; DB 2; Length 99;
Best Local Similarity 86.2%; Pred. No. 1.2e-35;
Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY      2  ESGPGLVKPAQTLSLSCAVSGGSGIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db      6  ESGPGLVKPSETLSLTCTVSGGSISSGGYWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

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QY      62  KSRIAMSVDTSENKFSRLNSVTAADTAVYVCAR 95
      |||||:|||||:|||||:|||||:|||||
Db      66  KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAR 99

RESULT 9
S09710
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains
A:Reference number: S09710; MUID:90262535; PMID:2111699
A:Accession: S09710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
A:Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match      74.3%; Score 452.5; DB 2; Length 146;
Best Local Similarity 68.3%; Pred. No. 2e-35;
Matches 84; Conservative 16; Mismatches 12; Indels 11; Gaps 2;

QY      2  ESGPGLVKPAQTLSLSCAVSGGSGIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db      25  ESGPGLVKPSETLSLTCTVSGGSGVSSGGLVWGWVQPPGKLEWIGSIFYSGNTYNNPSL 84

QY      62  KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG-----TLDIWGQGLTVT 111
Db      85  KSRVTISVDTLKNFSLKLSVTAADTAVYCYTR-PCYGDTSYRKRVMWMDLWGQGLTVT 143

QY      112 VSS 114
      |||
Db      144 VSS 146

RESULT 10
S44113
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S44113
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAW>
A:Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match      74.1%; Score 451.5; DB 2; Length 121;
Best Local Similarity 73.3%; Pred. No. 2e-35;
Matches 85; Conservative 13; Mismatches 15; Indels 3; Gaps 2;

QY      2  ESGPGLVKPAQTLSLSCAVSGGSGIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db      6  ESGPGLVKPSETLSLTCTVSGGSISSSYWGWVQPPGKLEWIGSIFYSGNTYNNPSL 65

QY      62  KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG--YT-LDIWGQGLTVTVSS 114
Db      66  KSRVTLSVDTSKNQFSLKLSVTAADTGVYVCSRLSGGYSDFDYWSQGLTVTVSS 121

```

RESULT 11

S31690

IG heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31690

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31690

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <CUI>

A:Cross-references: EMBL:Z14199; NID:g30984; PID:CNA78568.1; PID:g30985

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:20-102/Domain: immunoglobulin homology <IMM>

Query Match	74.1%	Score 451.5;	DB 2;	Length 130;
Best Local Similarity	72.1%	Pred. NO. 2.2e-35;		
Matches 88;	Conservative 11;	Mismatches 12;	Indels 11;	Gaps 2;

Qy	2	ESGFLVKPAQTLSUSCAVSGSRSRGYYWSWRQHPPKGLIEWGYIYHSGNTYNNPSL	61
Dd	11	ESGFLVKPSETLSITCTVSGSISS--YYNSWSRQPFGKLEWIGYIYVSGETNYNPSL	68
Qy	62	KSRIAMSVDTSENKPSRLNSVTAAATAVYICARLDG-----YILDIWGQGLTVTV	112
Dd	69	KSRVTISYDTSKNQPSLKLISSVTAADTAIVYCARGSSVLLMFEGELLYFDYWGGQLTVTV	128
Qy	113	SS 114    	
Dd	129	SS 130    	

## RESULT 12

SI19668  
Ig heavy chain V region (VH4DJH6) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
C:Accession: SI19668; S24445  
R:Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A:Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A:Reference number: SI19663; MUID:92085276; PMID:1748994  
A:Accession: SI19668  
A:Molecule type: mRNA  
A:Residues: 1-127 <NAR>  
A:Cross-references: EMBL:X61648  
R:Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24442  
A:Accession: S24445  
A:Molecule type: mRNA  
A:Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F' <ION>  
A:Cross-references: EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID:g1335380  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;  
Best Local Similarity 69.7%; Pred. No. 2.7e-35;  
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;

[illegible]

Qy	113	SS	114
Db	126	SS	127

RESULT 13

S09711  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S09711  
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and  
D;Reference number: S09710; PMID:90262535; PMID:2111699

A:Accession: S09711  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotrimer; immunoglobulin  
F:34:118/Domain: immunoglobulin homology <IM>

Query Match	74.0%;	Score 450.5;	DB 2;	Length 146;
Best Local Similarity	68.0%;	Pred. No. 3.1e-35;		
Matches 83;	Conservative 17;	Mismatches 13;	Indels 9;	Gaps 1

	QY	2	ESGFLVKPAQTLSLSCAVSGSIRGGYVWIRQHPOKGLGWLYIVHSGNTYYNSL	61
		:	:::::	:
		:	:::::	:
		:	:::::	:
		:	:::::	:
	DB	25	ESGFLVKPSETLSVTCTSGGSVSSGIYWIMRPPKGPGEWIGYIYSGTNYNSL	84
		:	:::::	:
		:	:::::	:
		:	:::::	:
		:	:::::	:
	QY	62	KSIAMSDVTSNKFSLRLNSTVAATAVVYCARL-----DGYTLDIHQGGQLTV	11
		:	:::::	:
		:	:::::	:
		:	:::::	:
		:	:::::	:
	PS	95	PSEVTTSVTSSKNQFSIKGVSTAAATAVYCARVLVSRTISIOXYMDWGKGTTVV	14
		:	:::::	:
		:	:::::	:
		:	:::::	:
		:	:::::	:

Qy	113	SS	114
Db	145	SS	146

## RESULT 14

S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of  
A:Reference number: S31509  
A:Accession: S31511  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PID:CAA49500.1; PID:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
R:47-129/Domains: immunoglobulin homology <IMM>

Query Match	73.8%;	Score 449.5;	DB 2;	Length 155;
Best Local Similarity	70.8%;	Pred. No. 4.1e-35;		
Matches	85;	Conservative 15;	Mismatches 11;	Indels 9;
Gaps	2;			

[illegible]

S31512  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31512  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A;Reference number: S31509  
A;Accession: S31512  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;47-129/domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 446.5; DB 2; Length 155;  
Best Local Similarity 70.0%; Pred. No. 7.8e-35;  
Matches 84; Conservative 16; Mismatches 11; Indels 9; Gaps 2;  
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYVWSWIRQHPGKLEWIGYVYHSGNTYVNP 61  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 61  
38 ESGPGLVKPSETLSLCTVSGSIS--YVWSWIRQPPGKLEWIGYVYVYTGSA 95  
QY 62 KSRVTSVDTSENKFSRLNSVTAADTAVVYCARLDG-----YTLDIWGQGLYTVSS 114  
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 114  
96 KSRVTSVDTSKNQFSLKSVTAADTAVVYCARGGISVYVYVYVYVYVYVYVYVYV 155

Search completed: August 8, 2004, 12:18:53  
Job time : 10.0182 secs

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Result No.	Score	Query %			DB	ID	Description
		Match	Length	DB			
1	419.5	68.9	129	1	HV2P HUMAN	P01824 homo sapien	
2	405	146	1	HV2I HUMAN	P06331 homo sapien		
3	374.5	61.5	137	1	HV4I MOUSE	P01822 mus musculus	
4	369.5	60.7	113	1	HV2G HUMAN	P01825 homo sapien	
5	361.5	59.4	113	1	HV47 MOUSE	P01823 mus musculus	
6	342.5	56.2	116	1	HV61 MOUSE	P18532 mus musculus	
7	341.5	56.1	116	1	HV60 MOUSE	P18531 mus musculus	
8	334	54.8	117	1	HV62 MOUSE	P18533 mus musculus	
9	321.5	52.8	144	1	HV43 MOUSE	P04819 mus musculus	
10	304	49.9	135	1	HV02 XENLA	P20957 xenopus lae	
11	300	49.3	120	1	HV2B HUMAN	P01815 homo sapien	
12	295	48.4	119	1	HV40 MOUSE	P01810 mus musculus	
13	293	48.1	122	1	HV3A HUMAN	P01762 homo sapien	
14	288	47.3	119	1	HV38 MOUSE	P01808 mus musculus	
15	285.5	46.9	119	1	HV2C HUMAN	P01816 homo sapien	
16	285	46.8	119	1	HV37 MOUSE	P01807 mus musculus	
17	282.5	46.4	121	1	HV3J HUMAN	P01771 homo sapien	
18	280.5	46.1	117	1	HV2B RABIT	P01828 cryptolagus	
19	278.5	45.7	125	1	HV2D HUMAN	P01817 homo sapien	
20	276	45.3	114	1	HV3B HUMAN	P01763 homo sapien	
21	275	45.2	122	1	HV3G HUMAN	P01768 homo sapien	
22	274.5	45.1	121	1	HV2E HUMAN	P01818 homo sapien	
23	274	45.0	116	1	HV05 CARAU	P19181 carassius a	
24	273	44.8	122	1	HV3H HUMAN	P01769 homo sapien	
25	272	44.7	114	1	HV2A RABIT	P01827 cryptolagus	
26	272	44.7	122	1	HV2I RABIT	P01790 mus musculus	
27	271	44.5	147	1	HV2H HUMAN	P04438 homo sapien	
28	270.5	44.4	115	1	HV3F HUMAN	P01767 homo sapien	
29	270.5	44.4	117	1	HV41 MOUSE	P01811 mus musculus	
30	270	44.3	115	1	HV44 MOUSE	P01820 mus musculus	
31	270	44.3	122	1	HV20 MOUSE	P01789 mus musculus	
32	269.5	44.3	142	1	HV01 RAT	P01805 rattus norv	
33	268.5	44.1	115	1	HV3D HUMAN	P01765 homo sapien	







```
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/CJ;
RX MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR: JTO508; HVMS1B.
DR PDB: 1KCS; 11-MAY-02.
DR PDB: 1KCV; 11-MAY-02.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 68 84 FRAMEWORK-3.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 56.2%; Score 342.5; DB 1; Length 116;
Best Local Similarity 69.1%; Pred. No. 9.1e-30;
Matches 65; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWISWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 24 ESGPDLVKPSQSLTCTVTGYSITS-GYSWIRQHPGKLEWIGYIYHSGNTYNPSSL 82

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR 95
DB 83 KSRIITRDTSKNQFLQNSVTTEDTATYICAR 116

Query Match 56.2%; Score 342.5; DB 1; Length 116;
Best Local Similarity 69.1%; Pred. No. 9.1e-30;
Matches 65; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWISWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 24 ESGPDLVKPSQSLTCTVTGYSITS-GYSWIRQHPGKLEWIGYIYHSGNTYNPSSL 82

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR 95
DB 83 KSRIITRDTSKNQFLQNSVTTEDTATYICAR 116

RESULT 7
HV60_MOUSE
ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/CJ;
RX MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: JTO509; HVMS31.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.

Query Match 56.2%; Score 342.5; DB 1; Length 116;
Best Local Similarity 69.1%; Pred. No. 9.1e-30;
Matches 65; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWISWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 24 ESGPDLVKPSQSLTCTVTGYSITS-GYSWIRQHPGKLEWIGYIYHSGNTYNPSSL 82

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR 95
DB 83 KSRIITRDTSKNQFLQNSVTTEDTATYICAR 116

RESULT 7
HV60_MOUSE
ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/CJ;
RX MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: JTO509; HVMS31.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
```

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FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 56.1%; Score 341.5; DB 1; Length 116;
Best Local Similarity 67.0%; Pred. No. 1.2e-29;
Matches 63; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWISWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 24 ESGPGLVKPSQSLTCTVTGYSITS-GYWNWIRQHPGKLEWIGYIYHSGNTYNPSSL 82

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR 95
DB 83 KNRISITRDTSKNQFLKNSVTTEDTATYICAR 116

RESULT 8
HV62_MOUSE
ID HV62_MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 733 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: JTO510; HVMS73.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 54.8%; Score 334; DB 1; Length 117;
Best Local Similarity 64.9%; Pred. No. 7.5e-29;
Matches 61; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWISWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 24 ESGPGLVKPSQSLTCTVTGYSITSITGNVRSWIRQHPGKLEWIGYIYHSGNTYNPSSL 83

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR 95
DB 84 KSRITITRDTSKNQFLNLSVTAEDTATYICAR 117

RESULT 9
HV43_MOUSE
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ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683 (1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8B47A7CB3706D30A CRC64;

Query Match 52.8%; Score 321.5; DB 1; Length 144;
Best Local Similarity 54.1%; Pred. No. 2.1e-27;
Matches 66; Conservative 21; Mismatches 24; Indels 11; Gaps 3;

QY 2 ESGFGLVKPAQTLSLSCAVSGGSIIRSGGYWWSIRQHPGKGLWIGYIHSGNTYINPSL 61
Db 25 ESGFGLVAPQSLSITCTVSGFSLT--GYGVNVRQPPGKGLWLTGIVNGSTDYNSTL 82

QY 62 KSRIMSVDTSENKFSRLNSVTAADTAIVYCA-----RIDGY-TLDIWGGTLVTV 112
Db 83 KSLRTIKDNGSKQVFLKMNLSQTDRTARYCASVSIYYGRSDKYFTLDYWGQTSVT 142

QY 113 SS 114
Db 143 SS 144

RESULT 10
HV02_XENLA
ID HV02_XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

```

```

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 49.9%; Score 304; DB 1; Length 135;
Best Local Similarity 51.3%; Pred. No. 1.4e-25;
Matches 59; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

QY 2 ESGFGLVKPAQTLSLSCAVSGGSIIRSGGYWWSIRQHPGKGLWIGYIHSGNTYINPSL 61
Db 23 ESGFGLVAPQSLSITCTVSGFSLS--YHMFVTRQPPGKGLWIGYIATGGSTAIADSL 80

QY 62 KSRIMSVDTSENKFSRLNSVTAADTAIVYCA--LDGY-TLDIWGGTLVTVSS 114
Db 81 KNRVTIKDNGKQVFLQMGMEVKDTAMYCYAREVAGYVFGQGTWTVTS 135

RESULT 11
HV2B_HUMAN
ID HV2B_HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660 (1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02089; GHUCO.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.

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GO; GO:0003823; F:antigen binding; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS0835; IG\_LIKE; 1.  
Immunoglobulin V region; Glycoprotein; Pyroglutamate carboxylic acid.  
DOMAIN 1 110  
FT MOD\_RES 1 1  
FT CARBOHYD 22 94  
FT DISULFID 62 62  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13226 MW; 158AB829AE7EEB98 CRC64;  
Query Match 49.3%; Score 300; DB 1; Length 120;  
Best Local Similarity 52.9%; Pred.No.3.4e-25;  
Matches 63; Conservative 16; Mismatches 30; Indels 10; Gaps 3;  
QY 2 ESGPGLVKPQTTLSLCAVSGSGSIRSGGYVSWIRQHPGKLEIGVYHSGNTYYPNSL 61  
DB 6 ESGPGLVKPQTTLTLCFTSGFSLSSTGCVGWIRQFPFGKLEWLARIDWDDKYYNTSL 65  
QY 62 KSRIAMSVDTSENKFSRLNSVTAADPAVYYCARLD-----GYTLDWGGTLVTVSS 114  
DB 66 ETRLTISKDSRQGVLTMDPV---DTATYTCARITVIPAPAGY-MDVWGRGTPVTVSS 120  
RESULT 12  
HV40 MOUSE STANDARD; PRT; 119 AA.  
ID HV40 MOUSE  
AC P01810;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ig heavy chain V region J539.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP PRELIMINARY SEQUENCE.  
RX MEDLINE=79223895; PubMed=111245;  
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;  
RT "Structural evidence for independent joining region gene in  
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and  
RT its potential role in generating diversity in  
RT complementarity-determining regions";  
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).  
RN [2]  
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
RL MEDLINE=88217852; PubMed=3449853;  
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,  
RA Davies D.R.;  
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction  
RT study at 2.6-A resolution.";  
RL Proteins 1:74-80 (1986).  
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS GALACTAN.  
PIR; A02080; AVMSJ5.  
PDB; 2PEJ; 15-OCT-90.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT NON\_TER 119 119  
FT STRAND 3 7  
FT STRAND 10 12  
FT TURN 14 15  
FT STRAND 18 25  
FT HELIX 29 31

Db 5 VQSGGLVKGPGSLRLSCVAGSFRD--FYMSWIRZTPGKGLZWVSYIGSGSTLYYAD 62  
 QY 60 SLKRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG-----YTLDIWQGTLYTVSS 114  
 Db 63 SVKGRFTISRDNQKSLYLZMBSLRTZBTAVYCAATBBPFWSTFSLBYWGZGBLTVTVSS 122

RESULT 14  
 HV38 MOUSE  
 ID HV38\_MOUSE STANDARD; PRT; 119 AA.  
 AC P01808;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE IG heavy chain V region T601.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79223895; PubMed=111245;  
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;  
 RT "Structural evidence for independent joining region gene in  
 RT immunoglobulin heavy chains from anti-galactan myeloma proteins and  
 RT its potential role in generating diversity in  
 RT complementarity-determining regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN  
 CC THAT BINDS GALACTAN.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02078; AVMS76.  
 DR HSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 47.3%; Score 288; DB 1; Length 119;  
 Best Local Similarity 52.6%; Pred. No. 6.4e-24;  
 Matches 61; Conservative 15; Mismatches 36; Indels 4; Gaps 3;  
 QY 1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSIRQHPGKLEWIGYIYHSGNTY-YNP 59  
 Db 5 LESGGLVQPGGSLKLSCAASGDF--SRYSMSVVRQAPGKLEWIGEINPDSTINYTP 62  
 QY 60 SLKRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG-YTLDIWQGTLYTVSS 114  
 Db 63 SLKDKFTISRDNKNTLYLQMSKVRSEDYALYCARLGYGYFDVWVGAGTLYTVSS 118

RESULT 15  
 HV2C HUMAN  
 ID HV2C\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01816;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE IG heavy chain V-II region DAW.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70258837; PubMed=5449120;  
 RA Press E.N., Hogg N.M.;  
 RT "The amino acid sequences of the Fd fragments of two human gamma-1

heavy chains."; Biochem. J. 117:641-660 (1970).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE  
 CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02091; GHUUDW.  
 DR HSP; P01789; IMCP.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 113 IG-LIKE.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 46.9%; Score 285.5; DB 1; Length 119;  
 Best Local Similarity 50.9%; Pred. No. 1.2e-23;  
 Matches 58; Conservative 18; Mismatches 37; Indels 1; Gaps 1;  
 QY 2 ESGGGLVKEAQTLSLSCAVSGGSIRSGGYWWSIRQHPGKLEWIGYIYHSGNTYINPSL 61  
 Db 6 ESGPALVRPTQTTLTCTFSGSLSGETMCVAMIRQPPGEALWLAWDILNDKDYGASL 65  
 QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG-YTLDIWQGTLYTVSS 114  
 Db 66 ETRLAVSKDISKNQVLSXNTVGFDTATYICARSCGSQYFDYWGQGLTVTVSS 119

Search completed: August 8, 2004, 12:14:31  
 Job time : 7.21818 secs



Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	473	77.7	478	4	Q7Z379		Q7Z379 homo sapien
2	451	74.1	150	4	O95973		O95973 homo sapien
3	446.5	73.3	119	4	Q9UL73		Q9UL73 homo sapien
4	432	70.9	496	4	O96KX8		O96KX8 homo sapien
5	430.5	70.7	492	4	Q7Z374		Q7Z374 homo sapien
6	430	70.6	613	4	O96EY0		O96EY0 homo sapien
7	409.5	67.2	588	4	Q8WUX4		Q8WUX4 homo sapien
8	409.5	67.2	597	4	O9BU10		O9BU10 homo sapien
9	409.5	67.2	618	4	Q96AA6		Q96AA6 homo sapien
10	408	67.0	139	4	O86SX2		O86SX2 homo sapien
11	405.5	66.6	597	4	O9BQB8		O9BQB8 homo sapien
12	405	66.5	130	4	O81ZD7		O81ZD7 homo sapien
13	388	63.7	473	4	O81C63		O81C63 homo sapien
14	377.5	62.0	479	11	Q99M22		Q99M22 mus musculus
15	374	61.4	116	4	Q7Z3Y6		Q7Z3Y6 homo sapien
16	362	59.4	122	4	O9UL75		O9UL75 homo sapien





```
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BX38077; CAD98001.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A1576F0CA74B CRC64;

  Query Match      70.7%; Score 430.5; DB 4; Length 492;
  Best Local Similarity 74.6%; Pred. No. 1.8e-36;
  Matches 83; Conservative 13; Mismatches 17; Indels 3; Gaps 2;

Qy 2 ESGGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 37 ESGGLVKPSETLSLTCVSGSVNRYWGWIRQPPGKLEWIGSYIYNENTYIYSPSL 96
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 KSRITMSVDTSENKFSRLNSVTAAADTAVYCAR-LDG--YTLDIWGQGLTVTVSS 114
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 97 KSLRTIFVDTSKNHFSLRLTSVTAADTAVYCVRHVEGPGYGFPGQGLTVTVSS 152
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC011857; AAH11857.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

  Query Match      70.6%; Score 430; DB 4; Length 613;
  Best Local Similarity 74.4%; Pred. No. 2.7e-36;
  Matches 89; Conservative 9; Mismatches 15; Indels 6; Gaps 2;

Qy 2 ESGGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 ESGGLVKPSETLSLTCVSGSIS--YYSWIRQHPAGKLEWIGRIYISGSYINPSSL 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 KSRITMSVDTSENKFSRLNSVTAAADTAVYCA----RLDGYTLDIWGQGLTVTVSS 114
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 KSRVTMSVDTSKNQFSLSKSLSVTAADTAVYCASQWELPTVGLFYWGQGLTVTVSS 139
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

  Query Match      67.2%; Score 409.5; DB 4; Length 597;
  Best Local Similarity 66.7%; Pred. No. 3.6e-34;
  Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSSLKS 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 GAGLLKPSSETLSLTCGYVGGSF--SGYYWSWIRQPPGKLEWIGEINHSGSTYNPSSLKS 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 64 RIAMSVDTSNKFSRLNSVTAAADTAVYCARL-----DG-YTLDIWGQGLTVTVSS 114
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RVTISVDTSKQLSLKLSVNAADTAVYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

  Query Match      67.2%; Score 409.5; DB 4; Length 597;
  Best Local Similarity 66.7%; Pred. No. 3.6e-34;
  Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSSLKS 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 GAGLLKPSSETLSLTCGYVGGSF--SGYYWSWIRQPPGKLEWIGEINHSGSTYNPSSLKS 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 64 RIAMSVDTSNKFSRLNSVTAAADTAVYCARL-----DG-YTLDIWGQGLTVTVSS 114
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RVTISVDTSKQLSLKLSVNAADTAVYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

  Query Match      67.2%; Score 409.5; DB 4; Length 597;
  Best Local Similarity 66.7%; Pred. No. 3.6e-34;
  Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;
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DR	PROSITE; PS08935; IG_LIKE; 1.
KW	plasmid.
FT	NON TER
SQ	SEQUENCE      1                  1 139 AA;     7D1E23202410E4F8C CRC64;
Query Match                      67.0%; Score 408; DB 4; Length 139; Best Local Similarity   80.9%; Pred.No.8.1e-35; Matches      76; Conservative   11; Mismatches   5; Indels    2; Gaps    1;	
Qy	2 ESGPGLVKPAQTLSLSCAVSNGGSIIRGGYVSWIROHPKGLEWGIVYHSGNTYNPSL 61   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   Db    38 ESGPGLVKPEITSLTCTVSIGSS--YYWSWIROPFGKGLEWIGIYGSTNYNPSL 95   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	62 KSRIAMSVDTSENKFSLRLNSVTAAATVAYVCAR 95   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	96 KSRVTISVDTSKNQFSKLSSVTAADTVAYVCAR 129   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
RESULT 11	
Q9BQB8	PRELIMINARY; PRT; 597 AA.
ID	Q9BQB8 AC Q9BQB8
AC	Q9BQB8
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB	Hypothetical protein.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Muscle, and Lymph;
RA	Straussberg R.;
RL	Submitted (APR.-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC006180; AAH06180.1; -.
DR	EBHL; BC001872; AAO1872.1; -.
DR	HSP; P01825; 7FAB.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 5.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS08935; IG_LIKE; 5.
DR	PROSITE; PS0290; IG_MHC; 3.
KW	Hypothetical protein_KW
SQ	SEQUENCE      597 AA;     2DAFAD50A6375851 CRC64;
Query Match                      66.6%; Score 405.5; DB 4; Length 597; Best Local Similarity   66.7%; Pred.No.9.4e-34; Matches      80; Conservative   13; Mismatches   16; Indels   11; Gaps    3;	
Qy	4 GPGLVPKPQAOTLSLSCAVSNGGSIIRGGYVSWIROHPKGLEWGIVYHSGNTYNPSLK 63   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	27 GAQLPKPETSLTCGVYGSF--SGYYSWIQPFPGKEWLGEINHGSHGNITYNPSLK 84   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	64 RIAMSVDTSENKFSLRLNSVTAAATVAYCARL-----DG-YTLDIWGQGTLVTVSS 114   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	85 RVTTISVDTSKKQLSKLSSNAADTVAYICARVITRASPTGDGRYGMVVGQGTTVTSS 144   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
RESULT 12	
Q8IZD7	PRELIMINARY; PRT; 130 AA.
ID	Q8IZD7 AC Q8IZD7
AC	Q8IZD7
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB	Anti-thyrogllobulin heavy chain variable region (Fragment).
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI TaxID=9606;

```

RN  SEQUENCE FROM N.A.
RP  Jang Y.-J., Chung J., Park J.-Y.;
RT  "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RL  Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL  Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY145445; AAN64329.1; -
DR  InterPro; IPR003599; IG-like.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; IG; 1.
DR  SMART; SM00409; IG; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
FT  NON_TER 1 130
FT  NON_TER 130 130
SQ  SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 66.5%; Score 405; DB 4; Length 130;
Best Local Similarity 65.6%; Pred. No. 1.5e-34;
Matches 82; Conservative 13; Mismatches 18; Indels 12; Gaps 4;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYYSWIRQHPGKLEWIGYIYHSGNT-----Y 56
Db 6 QSGPGLVKPSETLSLCTVSGSISSSSYWGIRQSPGKLEWIGSLYISSTYSGSPY 65

Qy 57 YNPISLKSRIAMSVTSENKFSRLNSVTAAATAVYYCA---RLDG---YT-LDIWGQGTLL 109
Db 66 YAPSLRGRVIRSVDTSKNQLSRLSSVTAAATAVYYCASPTHCSSGGGCGYAFFQWQGFL 125

Qy 110 VTSS 114
Db 126 VTSS 130

RESULT 13
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -
DR GO; GO:000507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER BLUE; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 63.7%; Score 388; DB 4; Length 473;
Best Local Similarity 65.2%; Pred. No. 4.7e-32;
Matches 75; Conservative 13; Mismatches 23; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61

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Db 32 ESGGLKPSVTLSLCTVSGDSVASSSYWGVRQPPGKLEWIGTINFGNMYSPSL 91
Qy 62 KSRIAMSVTSENKFSRLNSVTAAATAVYYCAR---LDGYTLDIWGQGTLLVTVS 113
Db 92 RSRVTMSADMSSENSFYKLDSVTAAATAVYYCAAGHLVMGFAGH-WGQGLVSVS 145

RESULT 14
Q99M22
ID Q99M22 PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002031; AAH02031.1; -
DR HSPF; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 62.0%; Score 377.5; DB 11; Length 479;
Best Local Similarity 64.9%; Pred. No. 6e-31;
Matches 74; Conservative 18; Mismatches 19; Indels 3; Gaps 3;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61
Db 24 ESGPGLVKPQSLSLCTCVTGYSTS-GYYWNWIRQFPGNKLEWNGVINYDGSNNYPSL 82

Qy 62 KSRIAMSVTSENKFSRLNSVTAAATAVYYCARLDGYT-LDIWGQGTLLVTVS 114
Db 83 KNRISTRDTSKNQFFLKLNSVTEDTATYYCAS-RGYSWFPNWWGQGTLLVTVA 135

RESULT 15
Q7Z3Y6
ID Q7Z3Y6 PRELIMINARY; PRT; 116 AA.
AC Q7Z3Y6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN VH4-34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tinguely M., Rosencuist R., Sundstroem C., Amini R.M., Koppers R.,
RA Hansmann M.L., Brauning A.;
RA "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT cell precursor in a germinal center.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -
FT NON_TER 1 1
FT NON_TER 1 1

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds  
(without alignments)  
688.123 Million cell updates/sec

Title: US-10-027-725A-7  
Perfect score: 609  
Sequence: 1 LESGPGLVKPAQTLSLCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	609	100.0	114	5	ABG30445 Human IGE
2	547	89.8	114	5	ABG30447 Human IGE
3	546	89.7	114	5	ABG30446 Human IGE
4	506.5	83.2	123	2	AAW78433 Antibody
5	506.5	83.2	123	5	ABR97976 Heavy cha
6	505	82.9	252	5	ABP45983 Human Bly
7	502	82.4	123	4	ABP62745 Human HIV
8	501.5	82.3	117	7	ABG39784 Anti-huma
9	501.5	82.3	117	7	ADD05388 Anti-MUC1
10	500.5	82.2	251	6	ABJ19829 Human VEG
11	499.5	82.0	120	4	AAAB62775 Human HIV
12	499	81.9	473	4	AAAB36206 Human imm
13	498.5	81.9	253	5	ABP45608 Human Bly
14	496	81.4	172	3	AA93713 The heavy
15	496	81.4	172	6	AAE35892 Human 2.1
16	495.5	81.4	122	4	AAAB62765 Human HIV
17	494.5	81.2	119	7	ADC99796 Anti-huma
18	494.5	81.2	119	7	ADD05400 Anti-MUC1
19	493.5	81.0	129	5	AAU81275 Human trk
20	490	80.5	126	3	ABP30584 A human v
21	490	80.5	126	5	ABP54970 Anti-idio
22	490	80.5	130	5	AAU81273 Human trk
23	490	80.5	251	5	ABG80712 Amyloid p
24	490	80.5	254	5	ABG80713 Amyloid p
25	490	80.5	263	5	ABG80714 Human Igg

26	489.5	80.4	117	7	ADC99776 Anti-huma
27	489.5	80.4	117	7	ADD05380 Anti-MUC1
28	489	80.3	118	2	AAAY06385 Humanised
29	483.5	79.4	129	5	AAU81276 Human trk
30	482	79.1	256	5	ABP45596 Human Bly
31	482	79.1	487	4	AAAB90607 Human sec
32	482	79.1	487	5	ABG65445 Human alb
33	481	79.0	246	3	AAAY15126 Anti-muri
34	479	78.7	118	2	AAAY06386 Humanised
35	477	78.3	118	2	AAAY06383 Humanised
36	476.5	78.2	117	7	ADC99804 Anti-huma
37	476.5	78.2	117	7	ADD05408 Anti-MUC1
38	474	77.8	252	5	ABP45318 Human Bly
39	474	77.8	256	5	ABP45734 Human Bly
40	473	77.7	229	3	AAAB30593 Variable
41	472.5	77.6	121	7	ADC99808 Anti-huma
42	472.5	77.6	121	7	ADD05412 Anti-MUC1
43	471.5	77.4	119	2	AAAR30143 MAB GAH v
44	471.5	77.4	119	2	AAW27554 Human Ab
45	471.5	77.4	119	6	ABP98691 Human GAH

## ALIGNMENTS

RESULT 1  
ABG30445  
ID ABG30445 standard; protein; 114 AA.  
XX AC ABG30445;  
XX AC  
DT 21-OCT-2002 (first entry)  
XX  
DE Human IGE Fab clone 94 heavy chain protein.  
XX  
KW Human; fab; anti-allergic; vaccine; grass pollen; PHI p 2;  
KW timothy grass pollen allergen; passive immunotherapy.  
XX  
OS Homo sapiens.

Key	Location/Qualifiers
Region	1..26
FT	/note= "FR1 region"
FT	27..33
FT	/note= "CDR1 region"
FT	34..47
FT	/note= "FR2 region"
FT	48..63
FT	/note= "CDR2 protein"
FT	64..95
FT	/note= "FR3 region"
FT	96..103
FT	/note= "CDR2 region"
FT	104..114
FT	/note= "FR4 region"

WO200253595-A1.

11-JUL-2002.

27-DEC-2001; 2001WO-SE002908.

29-DEC-2000; 2000SE-00004892.

(PHAA ) PHARMACIA DIAGNOSTICS AB.

Flicker S, Steinberger P, Kraft D, Valenta R;

WPI; 2002-583604/62.

N-ESDB; ABK89637.

Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

PS Disclosure; Page 36; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergenic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 94 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 100.0%; Score 609; DB 5; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-48;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGGLVKPAQTLSLCAVSGSIRSGYYWSWIRQHPKGLWIGYIYHSGNTYYNPS 60

Db 1 LESGGLVKPAQTLSLCAVSGSIRSGYYWSWIRQHPKGLWIGYIYHSGNTYYNPS 60

QY 61 LKSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLIDWGGTLVTVSS 114

Db 61 LKSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLIDWGGTLVTVSS 114

RESULT 2

ABG30447

ID ABG30447 standard; protein; 114 AA.

AC ABG30447;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 100 heavy chain protein.

XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95
FT Region	/note= "FR3 region"
FT Region	96..103
FT Region	/note= "CDR2 region"
FT Region	104..114
FT Region	/note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX

PR 29-DEC-2000; 2000SE-00004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

DR N-PSDB; ABK89639.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 38; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergenic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 100 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 89.8%; Score 547; DB 5; Length 114;

Best Local Similarity 89.5%; Pred. No. 1.1e-42;

Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LESGGLVKPAQTLSLCAVSGSIRSGYYWSWIRQHPKGLWIGYIYHSGNTYYNPS 60

Db 1 LESGGLVKPAQTLSLCAVSGSIRSGYYWSWIRQHPKGLWIGYIYHSGNTYYNPS 60

QY 61 LKSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLIDWGGTLVTVSS 114

Db 61 LKSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLIDWGGTLVTVSS 114

RESULT 3

ABG30446

ID ABG30446 standard; protein; 114 AA.

XX ABG30446;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 60 heavy chain protein.

XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95
FT Region	/note= "FR3 region"

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FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
FN WO200253595-A1.
FN 11-JUL-2002.
FF 27-DEC-2001; 2001WO-SE002908.
FF 29-DEC-2000; 2000SE-00004892.
FX (PHAA ) PHARMACIA DIAGNOSTICS AB.
FX Flicker S, Steinberger P, Kraft D, Valenta R;
FX WPI; 2002-583604/62.
FX N-PSDB; ABK89638.
FX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
FX variable region of group 2 allergen specific-human IgE Fabs, useful for
FX diagnosing or passive immunotherapy of type I allergy, for environmental
FX allergen detection.
FX Disclosure; Page 37; 45pp; English.
FX This invention relates to the DNA and protein sequences of group 2
FX allergen-specific human IgE Fabs and methods for their use. The proteins
FX of the invention may have antiallergic activities and may be used as a
FX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
FX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
FX 2 allergen-specific fabs of the invention may be useful for environmental
FX allergen detection and for standardisation of allergen extracts. The fabs
FX - or a vaccine againts a type I allergy is useful for passive
FX immunotherapy of type I allergy, it is also useful for diagnosing a type
FX I allergy. The allergen-specific fabs of the invention are useful for
FX inter alia, diagnosis, therapy and prevention of type I allergy. They are
FX also useful for identification of group 2 allergen-containing pollen and
FX may be used for blocking the binding of grass pollen allergic patients
FX IgE antibodies to Phi p 2. The present sequence represents the human IgG
FX fab, clone 60 heavy chain protein of the invention
SQ Sequence 114 AA;
Query Match 89.7%; Score 546; DB 5; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.4e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
Qy 1 LESGFLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIHSGNTYINPS 60
Db 1 LESGFLVKPQSQTLSLCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIHSGNTYINPS 60
Qy 61 LKSRIMSVDTSENKFSRLNSVTAADTAVYVCARLDGYTLIDWGQGLTVTVSS 114
Db 61 LKSRITVSDTSKNHFSRLTSLVTAADTAVYVCARSDGYTLIDNWGQGLTVTVSS 114
RESULT 4
AAW78433
XX AAW78433 standard; protein; 123 AA.
AC AAW78433;
XX AAW78433;
DT 11-MAY-1999 (first entry)
XX Antibody heavy chain targeted to obr clone 26.
DE Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
XX Synthetic.
XX

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PN WO9850431-A2.
XX 12-NOV-1998.
XX 30-APR-1998; 98WO-US008762.
XX 02-MAY-1997; 97US-00850058.
PR 24-JUN-1997; 97US-0050661P.
XX (GETH ) GENENTECH INC.
XX Arathoon R, Carter PJ, Merchant AM, Presta LG;
XX WPI; 1999-070091/06.
XX Selective preparation of multispecific antibodies - with heteromultimeric
XX heavy chain and common light chain components, useful for, e.g. in vivo
XX diagnosis of cancer.
XX Example 4; Fig 5; 69pp; English.
XX This sequence represents the heavy chain variable region for an antibody
XX that binds to the obr clone 26 protein. The sequence encoding the chain
XX is generated by a new method for preparing a multispecific Ab comprising
XX a first polypeptide (pp) and at least 1 extra pp, where: (i) the first pp
XX comprises a multimerisation domain (MD) forming an interface positioned
XX to interact with an interface of a MD of the extra pp; and (ii) the first
XX and extra pps each have a binding domain, which comprises a heavy chain
XX and a light chain, where the variable light chains of the first and extra
XX pps comprise a common sequence. The method comprises: (a) culturing a
XX host cell comprising nucleic acid encoding the first pp and extra pp, and
XX the variable light chain, such that the nucleic acid is expressed; and
XX (b) recovering the multispecific Ab from the culture. The method prepares
XX heteromultimeric pps, such as bispecific Abs, bispecific immunoadhesins
XX and Ab-immunoadhesin chimeras. The method allows for the enhanced
XX formation of the desired heteromultimer relative to the undesired
XX heteromultimers and homomultimers. The Abs can be used in immunoassays
XX and for the in vitro or in vivo diagnosis of various diseases, such as
XX cancer
SQ Sequence 123 AA;
Query Match 83.2%; Score 506.5; DB 2; Length 123;
Best Local Similarity 79.0%; Pred. No. 6.5e-39;
Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
Qy 1 LESGFLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIHSGNTYINPS 60
Db 5 VESGFLVKPQSQTLSLCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYSGTYINPS 64
Qy 61 LKSRIMSVDTSENKFSRLNSVTAADTAVYVCARLD-----GYTLIDWGQGLTVTVSS 114
Db 65 LKSRVITSDTSKNQFSLKLSVTAADTAVYVCARVLDYDYGSGASDYWGQGLTVTVSS 123
RESULT 5
ABB97976
ID ABB97976 standard; protein; 123 AA.
XX ABB97976;
AC ABB97976;
DT 06-SEP-2002 (first entry)
XX Heavy chain variable region from antibody obr.26.
DE Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
KW antiviral; vaccine; tumour.
XX Synthetic.
OS US2002062010-A1.
XX 23-MAY-2002.
XX

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XX 23-MAY-2001; 2001US-00863693.
XX
XX 02-MAY-1997; 97US-0046816P.
XX 30-APR-1998; 98US-00070166.
XX (GETH ) GENENTECH INC.
XX
XX Arathoon WR, Carter PJ, Merchant AM, Presta LG;
XX
XX WPI; 2002-499676/53.
XX
XX New multispecific antibodies having heteromultimeric and common
XX components are useful to direct treatment to a target site such as a
XX tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
XX treat infectious disease.
XX
XX Example 4; Fig 5; 36pp; English.
XX
XX The invention relates to a new multispecific antibody, comprising at
XX least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1
XX has a multimerisation domain forming an interface positioned to interact
XX with an interface of a multimerisation domain of PP2, and both
XX polypeptides each comprise a binding domain consisting a heavy chain and
XX a variable light chain, where the light chain has a sequence common to
XX both polypeptides. Heteromultimers of the inventions include bispecific
XX antibodies, bispecific immunoadhesins and antibody-immunoadhesin
XX chimeras. The activity of antibodies of the invention may be described
XX as, cytostatic, antibacterial and antiviral. The heteromultimer can be
XX used for redirected cytotoxicity, for example to kill tumour cells, as a
XX vaccine adjuvant, for delivering thrombolytic agents to clots, for
XX converting enzyme activated prodrugs at a target site such as a tumour,
XX for treating infectious diseases, for targeting immune complexes to cell
XX surface receptors or for delivering immunotoxins to tumour cells. The
XX current sequence represents the heavy chain variable region from antibody
XX obr.26 used in the construction of bispecific antibodies
XX
XX Sequence 123 AA;
XX
XX Query Match 83.2%; Score 506.5; DB 5; Length 123;
XX Best Local Similarity 79.0%; Pred. No. 6.5e-39;
XX Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;
XX
XX QY 1 LKSGPLVKPAQTLSLSCAVSGGSIKSGYYSWIRQHPKGLWIGYIYHSGNTYVNS 60
XX as :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 5 VESGGLVKPQTLSTCTVSGGSIKSGYYSWIRQHPKGLWIGYIYHSGNTYVNS 64
XX
XX QY 61 LKSRVITSDTSENKPSLRLNSVTAADTAVYYCARLD-----GYTLDIWGQGLTVTVSS 114
XX ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 65 LKSRVITSDTSENKPSLRLNSVTAADTAVYYCARLDYDYGSGADYWGQGLTVTVSS 123
XX
XX RESULT 6
XX ABP45983
XX ID ABP45983 standard; protein; 252 AA.
XX
XX AC ABP45983;
XX
XX XX 19-AUG-2002 (first entry)
XX
XX DE Human BlyS binding scFv SEQ ID 1994.
XX
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX OS Homo sapiens.
XX
XX XX WO200202641-A1.
XX
XX
XX
XX

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PD 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2779-2780; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 252 AA;
XX
XX Query Match 82.9%; Score 505; DB 5; Length 252;
XX Best Local Similarity 78.2%; Pred. No. 1.9e-38;
XX Matches 93; Conservative 12; Mismatches 8; Indels 6; Gaps 1;
XX
XX QY 2 ESGPGLVKPAQTLSLSCAVSGGSIKSGYYSWIRQHPKGLWIGYIYHSGNTYVNSL 61
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 6 ESGPGLVKPQTLSTCTVSGGSIKSGYYSWIRQHPKGLWIGYIYHSGNTYVNSL 65
XX
XX QY 62 KSRVITSDTSENKPSLRLNSVTAADTAVYYCARL-----DGYTLDIWGQGLTVTVSS 114
XX ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 66 KSRVITSDTSENKPSLRLNSVTAADTAVYYCARLDPADYDYGDFYWGQGLTVTVSS 124
XX
XX RESULT 7
XX AAB62745
XX ID AAB62745 standard; protein; 123 AA.
XX
XX AC AAB62745;
XX
XX XX 03-APR-2001 (first entry)
XX
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis.
XX
XX OS Homo sapiens.
XX
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX

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XX 23-JUN-2000; 2000WO-US017327.
XX PF
XX 30-JUN-1999; 99US-0141701P.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Watkins BA, Reitz MS;
XX PI
XX WPI; 2001-112438/12.
XX DR
XX N-PSDB; AAF29046.
XX PR
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal.
XX PS
XX Claim 1; Page 50; 81pp; English.
XX CC
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection
XX CC
XX Sequence 123 AA;
XX SQ
XX
XX Query Match 82.4%; Score 502; DB 4; Length 123;
XX Best Local Similarity 79.5%; Pred. No. 1.7e-38;
XX Matches 93; Conservative 11; Mismatches 9; Indels 4; Gaps 1;
XX
XX 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWMSWIRQHPGKLEWIGYIYHSGNTYYPNSL 61
XX 7 ESGPGLVKPQTLSLTCTVSGGSIIRSGGYWMSWIRQHPGKLEWIGYIYHSGNTYYPNSL 66
XX
XX 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARL-----DGYTLIDWGQGLTVTVSS 114
XX 67 KSRVTISIDTSKNKFSKLSVTAADTAVYYCARAAVCGGDCSFDYNGQGLTVTVSS 123
XX
XX
XX RESULT 8
XX ADC99784
XX ID ADC99784 standard; protein; 117 AA.
XX AC
XX ADC99784;
XX
XX 01-JAN-2004 (first entry)
XX
XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.
XX
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytotstatic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human.
XX
XX Homo sapiens.
XX
XX WO2003057838-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
XX
XX 28-DEC-2001; 2001US-0346299P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J;
XX
XX WPI; 2003-587113/55.
XX
XX N-PSDB; ADC99786.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
XX or condition associated with expression of MUC18 in a patient, e.g.
XX
XX tumors, cancers, and other malignancies.
XX
XX Claim 1; SEQ ID NO 13; 78pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
XX a heavy or light chain amino acid or a heavy or light chain variable
XX domain where the antibody binds to MUC18. The monoclonal antibody of the
XX invention demonstrates cytostatic activity and may be useful for treating
XX a disease or condition associated with the expression of MUC18 on the
XX cell surface such as tumours, specifically melanoma, oesophageal,
XX pancreatic or colorectal tumours, carcinomas, particularly cervical
XX carcinomas and cervical intraepithelial neoplasia and cancers including
XX colorectal, breast or lung cancer, as well as other malignancies. The
XX current sequence is that of the anti-human MUC18 monoclonal antibody
XX heavy chain protein of the invention.
XX
XX Sequence 117 AA;
XX SQ
XX
XX Query Match 82.3%; Score 501.5; DB 7; Length 117;
XX Best Local Similarity 81.4%; Pred. No. 1.8e-38;
XX Matches 92; Conservative 13; Mismatches 7; Indels 1; Gaps 1;
XX
XX 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWMSWIRQHPGKLEWIGYIYHSGNTYYPNSL 61
XX 6 ESGPGLVKPQTLSLTCTVSGGSIIRSGGYWMSWIRQHPGKLEWIGYIYHSGNTYYPNSL 65
XX
XX 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDGYTLIDWGQGLTVTVSS 114
XX 66 KSRVTISIDTSKNKFSKLSVTAADTAVYYCAR-EGDGFYWGQGLTVTVSS 117
XX
XX
XX RESULT 9
XX ADD05388
XX ID ADD05388 standard; protein; 117 AA.
XX AC
XX ADD05388;
XX
XX 01-JAN-2004 (first entry)
XX
XX Anti-MUC18 antibody heavy chain variable region protein, SEQ ID NO 13.
XX
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
XX
XX Homo sapiens.
XX
XX WO2003057006-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
XX 28-DEC-2001; 2001US-0346460P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Bar-Eli M;
XX
XX WPI; 2003-577496/54.
XX
XX N-PSDB; ADD05390.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX associated with melanoma, or increasing survival of an animal having a
XX metastatic tumor.
XX
XX Claim 1; SEQ ID NO 13; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumour growth in an animal. The tumour inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
```

CC amino acids given in the specification, and where the monoclonal antibody  
CC binds MUC18, and contacting the tumour with the antibody resulting in  
CC inhibited proliferation of the cells. The monoclonal antibody has  
CC cytostatic and can be used in the production of a vaccine. The monoclonal  
CC antibodies against the MUC18 antigen are useful for diagnosing and  
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
CC increasing survival of an animal having a metastatic tumour. This  
CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
CC protein of the invention.

XX SQ Sequence 117 AA;  
Query Match 82.3%; Score 501.5; DB 7; Length 117;  
Best Local Similarity 81.4%; Pred. No. 1.8e-38;  
Matches 92; Conservative 13; Mismatches 7; Indels 1; Gaps 1;  
QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGYMSWIRQHPGKLEWIGYIYHSGTYNPSL 61  
DB 6 ESGPGLVPAQTLSLSCAVSGSIRSGYMSWIRQHPGKLEWIGYIYHSGTYNPSL 65  
QY 62 KSRIAMSVDTSENKSLRLNSVTAAATVAVYCARLDGYTLDIWGGTGLTVVSS 114  
DB 66 KSRVTISVDTSKNQFSLKSLSSVTAAATVAVYCAR-EGDGFYWGOGTGLTVVSS 117

RESULT 10  
ABU19829  
ID ABU19829 standard; protein; 251 AA.  
XX AC ABU19829;  
XX DT 10-APR-2003 (first entry)  
XX DE Human VEGF-2 related protein SEQ ID No 75.  
XX KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic;  
KW antiarthritic; antidiabetic; ophthalmological; antiallergic;  
KW immunosuppressive; dermatological; antipsoriatic; vulnery; antibody;  
KW CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;  
KW proliferative disorder; cardiovascular disorder; arrhythmia;  
KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;  
KW infectious disease; autoimmune disease; rheumatoid arthritis;  
KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;  
KW angiogenesis; wound healing; vascular tissue repair; human.

XX OS Homo sapiens.  
XX XX  
XX PN WO200283704-A1.  
XX XX  
XX PD 24-OCT-2002.  
XX PF 12-APR-2002; 2002WO-US011474.  
XX XX  
XX PR 13-APR-2001; 2001US-0283385P.  
XX PR 24-JAN-2002; 2002US-0350366P.  
XX XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX XX  
XX PI Rosen CA, Albert VR, Ruben SM, Wager RE;  
XX XX  
XX DR WPI; 2003-092991/08.

XX PT New isolated polynucleotide encoding an antibody which inhibits a VEGF-2  
PT polypeptide, useful for diagnosing, treating or preventing diseases  
PT associated with aberrant VEGF-2 expression or function, e.g. cancer or  
PT inflammation.  
XX PT  
XX PS Disclosure; Page 385-386; 425pp; English.  
XX XX  
XX CC The invention relates to an isolated polynucleotide encoding a first  
CC antibody at least 95-100% identical to a second antibody comprising an  
CC amino acid sequence selected from at least one, two or three CDR

CC region(s) of a VH or VL domain where the first antibody  
CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated  
CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,  
CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or  
CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,  
CC such as cancer and other proliferative disorders, cardiovascular  
CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral  
CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases  
CC (e.g. rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),  
CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and  
CC antibodies may also be used to stimulate angiogenesis, wound healing, and  
CC promoting vascular tissue repair. The polynucleotide and polypeptide may  
CC also be used for in vitro purposes related to scientific research,  
CC synthesis of DNA and manufacture of DNA vectors, and for the production  
CC of diagnostics and therapeutics to treat human diseases. This sequence  
CC represents a human VEGF-2 related protein of the invention

XX SQ Sequence 251 AA;  
Query Match 82.2%; Score 500.5; DB 6; Length 251;  
Best Local Similarity 79.7%; Pred. No. 5e-38;  
Matches 94; Conservative 13; Mismatches 6; Indels 5; Gaps 2;  
QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGYMSWIRQHPGKLEWIGYIYHSGTYNPSL 61  
DB 6 ESGPGLVPAQTLSLSCAVSGSIRSGYMSWIRQHPGKLEWIGYIYHSGTYNPSL 65  
QY 62 KSRIAMSVDTSENKSLRLNSVTAAATVAVYCAR---LDGYT--LDIWGGTGLTVVSS 114  
DB 66 KSRITMSVDTSKNQFSLKSLSSVTAAATVAVYCARDKVVTGSGDFLWGRGTLTVVSS 123

RESULT 11  
AAB62775  
ID AAB62775 standard; protein; 120 AA.  
XX AC AAB62775;  
XX DT 03-APR-2001 (first entry)  
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
KW envelope glycoprotein; gp120; diagnosis.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX PN WO200100678-A1.  
XX XX  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-US017327.  
XX PR 30-JUN-1999; 99US-0141701P.  
XX XX  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX XX  
XX PI Watkins BA, Reitz MS;  
XX XX  
XX DR WPI; 2001-112438/12.  
XX DR N-PSDB; AAF29076.

XX PT Novel human monoclonal antibody immunoreactive with human  
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
PT in biological sample and providing passive immunotherapy to HIV-1  
PT infected mammal.  
XX PT  
XX PS Claim 1; Page 69; 81pp; English.  
XX CC  
XX CC The present invention provides the protein and coding sequences for the  
CC variable regions of human monoclonal antibodies which are immunoreactive  
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
CC These can be used in diagnosis and therapy of HIV-1 infection

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XX SQ Sequence 120 AA;
Query Match 82.0%; Score 499.5; DB 4; Length 120;
Best Local Similarity 81.0%; Pred. No. 2.8e-38;
Matches 94; Conservative 12; Mismatches 5; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 7 ESGPGLVKPSQLSLTCTVSGSISGGYWSWIRQHPGKLEWIGYIYSGSTYNPSSL 66
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCAR---LDGYTLDIWGQGLTVTVSS 114
DB 67 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARGVVDWF--DPWGQGLTVTVSS 120

RESULT 12
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX AC AAB36206;
XX DT 15-FEB-2001 (first entry)
XX DE Human immune system associated protein HISAP-4.
XX KW Human; immune system associated protein; HISAP-4; immune disorder;
XX KW infection; autoimmune disease; cancer.
XX OS Homo sapiens.
XX PN US6135941-A.
XX PD 24-OCT-2000.
XX PF 27-MAR-1998; 98US-00049672.
XX PR 27-MAR-1998; 98US-00049672.
XX PA (INCYTE) INCYTE PHARM INC.
XX PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
XX PI Hillman JL, Au-Young J;
XX DR WPI: 2001-030926/04.
XX DR N-PSDB; AAC66522.
XX PS Claim 1; Col 53-56; 54pp; English.
XX CC The present invention provides the coding and protein sequences for a
XX CC number of human immune system associated proteins (HISAPs). These can be
XX CC used in the diagnosis and treatment of various autoimmune disorders,
XX CC infections and cell proliferation diseases. The diseases include AIDS,
XX CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
XX CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
XX CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
XX CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX SQ Sequence 473 AA;
Query Match 81.9%; Score 499; DB 4; Length 473;
Best Local Similarity 78.2%; Pred. No. 1.3e-37;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
DB 25 ESGPGLVKPSQLSLTCTVSGSISGGYWSWIRQHPGKLEWIGYIYSGSTYNPSSL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLD-----GYTLDIWGQGLTVTVSS 114

DB 85 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCARDVGLRGNGYGMVWGQGLTVTVSS 143

RESULT 13
ABP45608
ID ABP45608 standard; protein; 253 AA.
XX AC ABP45608;
XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 1619.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KW anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX DR WPI: 2002-114799/15.
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2335-2336; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX CC and so may be used to detect and quantitate the presence of BlyS in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of BlyS. They may also be
XX CC administered to treat diseases associated with aberrant BlyS expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX CC the antibodies and fragments of the antibodies described in the method of
XX CC the invention
XX SQ Sequence 253 AA;
Query Match 81.9%; Score 498.5; DB 5; Length 253;
Best Local Similarity 77.9%; Pred. No. 7.6e-38;
Matches 95; Conservative 12; Mismatches 6; Indels 9; Gaps 3;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWSWIRQHPGKLEWIGYIYHSGNTYNPSSL 61
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Db 6 ESGPLVKPSQTLTSLCTVSGGSISSGGYVWSWIRHPKGLWIGYIYSGSYNPSL 65  
Qy 62 KSRVTSVDTSENKFSRLNSVTAAADTAATVYCAR-----LDG--YT--LDIWGGGLTVTV 112  
Db 66 KSRVTISDTSKNQFSLKSLSSVTAADTAATVYCVRSYDILTRPVTADFIDWKGGLTVTV 125  
Qy 113 SS 114  
Db 126 SS 127

RESULT 14  
AAV93713  
ID AAV93713 standard; protein; 172 AA.  
AC AAV93713;  
XX  
XX  
DT 03-OCT-2000 (first entry)  
DE The heavy chain of immunoglobulin clone 2.1.1.3.  
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
KW proliferative disorder; cancer; immunodeficient disorder.  
XX Homo sapiens.  
OS  
XX WO200037504-A2.  
PN  
XX  
PD 29-JUN-2000.  
PF 23-DEC-1999; 99WO-US030895.  
XX  
PR 23-DEC-1998; 98US-0113647P.  
XX  
XX (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
PI Corvalan JR;  
PI  
XX  
XX WPI; 2000-442647/38.  
DR N-PSDB; AAA46876.  
XX  
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)  
PT -4 containing specified heavy and light chain sequences, useful for  
PT treating, e.g. immune disorders.  
XX  
XX Claim 2; Fig 1G; 157pp; English.  
XX  
XX The present sequence represents a heavy chain of an antibody of the  
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)  
CC -4. Antibodies of the invention are composed of a heavy chain variable  
CC region, comprising a modified contiguous sequence from a FRI-FR3 sequence  
CC encoded by a human VH3-33 family gene. The modifications are contained in  
CC CDRI, CD2 and/or framework regions. The antibodies may be used to  
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity  
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and  
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be  
CC used to up-regulate immune system to up-regulate immunodeficient  
CC disorders  
XX  
SQ Sequence 172 AA;  
Query Match 81.4%; Score 496; DB 3; Length 172;  
Best Local Similarity 79.8%; Pred. No. 8.6e-38;  
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;  
Qy 3 SGPLVKPAQTLTSLSCAVSGSIRSGGYVWSWIRHPKGLWIGYIYSGSYNPSL 62  
Db 1 SGPLVKPSQTLTSLCTVSGGSISSGGYVWSWIRHPKGLWIGYIYSGSYNPSL 60  
Qy 63 SRIAMSVDTSENKFSRLNSVTAAADTAATVYCARLDG--YTLDIWGGGLTVTVSS 114

Db 61 SRVTISVDTSKNQFSLKSLSSVTAADTAATVYCARDSGDYVGDVWGQGLTVTVSS 114  
RESULT 15  
AAE35892  
ID AAE35892 standard; protein; 172 AA.  
XX  
XX AAE35892;  
XX  
DT 17-JUN-2003 (first entry)  
DE Human 2.1.1.3 anti-CTLA-4 antibody heavy chain.  
XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;  
KW cancer.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Region 24..31  
FT /note= "Complementarity determining region (CDR) 1"  
FT Region 45..61  
FT /note= "Complementarity determining region (CDR) 2"  
FT Region 94..103  
FT /note= "Complementarity determining region (CDR) 3"  
XX  
XX EPI262193-A1.  
PN  
XX  
PD 04-DEC-2002.  
XX  
XX 23-MAY-2002; 2002EP-00253652.  
XX  
XX 23-MAY-2001; 2001US-0293042P.  
XX  
XX (PFIZ ) PFIZER PROD INC.  
PI Hanson DC, Mueller EE;  
XX  
XX WPI; 2003-131215/13.  
DR  
XX  
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the  
PT preparation of medicament for the treatment of cancer.  
PT  
XX  
XX Disclosure; Fig 3; 76pp; English.  
XX  
XX The invention relates to the use of human anti-cytotoxic T lymphocyte  
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for  
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin  
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian  
CC cancer, cancer of the anal region, stomach cancer, breast cancer,  
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.  
CC The present sequence is human anti-CTLA-4 antibody heavy chain  
XX  
SQ Sequence 172 AA;  
Query Match 81.4%; Score 496; DB 6; Length 172;  
Best Local Similarity 79.8%; Pred. No. 8.6e-38;  
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;  
Qy 3 SGPLVKPAQTLTSLSCAVSGSIRSGGYVWSWIRHPKGLWIGYIYSGSYNPSL 62  
Db 1 SGPLVKPSQTLTSLCTVSGGSISSGGYVWSWIRHPKGLWIGYIYSGSYNPSL 60  
Qy 63 SRIAMSVDTSENKFSRLNSVTAAADTAATVYCARLDG--YTLDIWGGGLTVTVSS 114  
Db 61 SRVTISVDTSKNQFSLKSLSSVTAADTAATVYCARDSGDYVGDVWGQGLTVTVSS 114

Search completed: August 8, 2004, 12:13:45  
Job time : 48.8091 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 38.5182 Seconds  
(without alignments)  
928.389 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	609	100.0	114	14	US-10-027-725A-7
2	556	91.3	114	14	US-10-027-725A-9
3	546	89.7	114	14	US-10-027-725A-8
4	519	85.2	122	15	US-10-309-762-147
5	518.5	85.1	121	15	US-10-309-762-152
6	517.5	85.0	125	15	US-10-309-762-11
7	514.5	84.5	121	15	US-10-309-762-151
8	512	84.1	118	15	US-10-309-762-138
9	512	84.1	120	15	US-10-309-762-13
10	512	84.1	120	15	US-10-309-762-144
11	509.5	83.7	123	15	US-10-309-762-12
12	508.5	83.5	123	15	US-10-309-762-10
13	508.5	83.5	123	15	US-10-309-762-18
14	508.5	83.5	123	15	US-10-309-762-19
15	508.5	83.5	125	15	US-10-309-762-8

16	508.5	83.5	125	15	US-10-309-762-16
17	506.5	83.2	119	15	US-10-309-762-131
18	505.5	83.0	119	15	US-10-309-762-140
19	505	82.9	252	10	US-09-880-748-1994
20	505	82.8	252	12	US-10-293-418-1994
21	504.5	82.8	125	15	US-10-309-762-153
22	504	82.8	120	15	US-10-309-762-139
23	503.5	82.7	127	15	US-10-309-762-14
24	503	82.6	124	15	US-10-309-762-75
25	503	82.6	143	15	US-10-309-762-96
26	501.5	82.3	117	14	US-10-330-613-13
27	501.5	82.3	117	14	US-10-330-530-13
28	501.5	82.3	117	16	US-10-660-357-13
29	500.5	82.2	251	14	US-10-120-414-75
30	498.5	81.9	253	10	US-09-880-748-1619
31	498.5	81.9	253	12	US-10-293-418-1619
32	497	81.6	110	15	US-10-309-762-74
33	497	81.6	121	12	US-10-453-698-137
34	497	81.6	121	15	US-10-308-817-137
35	496.5	81.5	123	15	US-10-309-762-17
36	496	81.4	172	14	US-10-153-382-21
37	495.5	81.4	123	15	US-10-309-762-9
38	494.5	81.2	119	14	US-10-330-613-25
39	494.5	81.2	119	14	US-10-330-530-25
40	494.5	81.2	119	16	US-10-660-357-25
41	493.5	81.0	129	16	US-10-312-316-47
42	493	81.0	221	10	US-09-972-656-80
43	490	80.5	126	9	US-09-974-449-6
44	490	80.5	130	16	US-10-312-316-45
45	489.5	80.4	117	14	US-10-330-613-5

#### ALIGNMENTS

#### RESULT 1

US-10-027-725A-7  
; Sequence 7, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match	100.0%	Score	609;	DB	14;	Length	114;
Best Local Similarity	100.0%	Pred. No.	2.9e-50;	Mismatches	0;	Indels	0;
Matches	114;	Conservative	0;	0;	0;	Gaps	0;
Qy	1	LES	GPGLVKPAQTLSLSCAVSGGSIRSGGYWWSIRQHPGKLEWIGYVYHSGNTYNPS	60			
Db	1	LES	GPGLVKPAQTLSLSCAVSGGSIRSGGYWWSIRQHPGKLEWIGYVYHSGNTYNPS	60			
Qy	61	LK	SIAMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLDIWGQGLTVTVSS	114			
Db	61	LK	SIAMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLDIWGQGLTVTVSS	114			

#### RESULT 2

US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

```
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match
Best Local Similarity 91.3%; Score 556; DB 14; Length 114;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPS 60
Db 1 LESGGLVKPQSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPS 60
QY 61 LKSRIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 114
Db 61 LKSRTVMSVDTSKNHFSLRLSSVTAADTAIVYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match
Best Local Similarity 89.7%; Score 546; DB 14; Length 114;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LESGGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPS 60
Db 1 LESGGLVKPQSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPS 60
QY 61 LKSRIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 114
Db 61 LKSRTVMSVDTSKNHFSLRLSSVTAADTAIVYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

```
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match
Best Local Similarity 85.2%; Score 519; DB 15; Length 122;
Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPQSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 122

RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match
Best Local Similarity 81.9%; Score 518.5; DB 15; Length 121;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPQSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYYNPSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAIVYCARLDGYTLDIWGQGLTVTVSS 121

RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

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; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11

Query Match      85.0%; Score 517.5; DB 15; Length 125;
Best Local Similarity 81.7%; Pred. No. 1.6e-41;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

Qy  2  ESGPGLVKPAQTLSLSCAVSGGSRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNP 61
Db  6  ESGPGLVKPQTLSLTCVSGGSISSGGYYWSWIRQHPGKLEWIGYIYHSGNTYYNP 65

Qy  62  KSRIAMSVDTSENKFSRLNSVTAADTAVYYCAR---LDGY--TLDIWGQGLTVTVSS 114
Db  66  KSRITISVDTSKNQFSLKSLSVTAADTAVYYCARTYYDFLTGYPDAFDIWGQGLTVTVSS 125

RESULT 7
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151

Query Match      84.5%; Score 514.5; DB 15; Length 121;
Best Local Similarity 81.0%; Pred. No. 2.9e-41;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;

Qy  2  ESGPGLVKPAQTLSLSCAVSGGSRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNP 61
Db  6  ESGPGLVKPQTLSLTCVSGGSISSGGYYWSWIRQHPGKLEWIGYIYHSGNTYYNP 65

Qy  62  KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARL---DGYTLDIWGQGLTVTVSS 114
Db  66  KSRVITISVDTSKNQFSLKSLSVTAADTAVYYCARVLLWFGYGMVDWVGQGLTVTVSS 121

RESULT 8
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      84.1%; Score 512; DB 15; Length 118;
Best Local Similarity 83.2%; Pred. No. 4.9e-41;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy  2  ESGPGLVKPAQTLSLSCAVSGGSRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNP 61
Db  6  ESGPGLVKPQTLSLTCVSGGSISSGGYYWSWIRQHPGKLEWIGYIYHSGNTYYNP 65

Qy  62  KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDGYTLDIWGQGLTVTVSS 114
Db  66  KSRVITISVDTSKNQFSLKSLSVTAADTAVYYCARYYGGSDYWGQGLTVTVSS 118

RESULT 9
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      84.1%; Score 512; DB 15; Length 120;
Best Local Similarity 81.9%; Pred. No. 5e-41;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

Qy  2  ESGPGLVKPAQTLSLSCAVSGGSRSGGYYSWIRQHPGKLEWIGYIYHSGNTYYNP 61
Db  6  ESGPGLVKPQTLSLTCVSGGSISSGGYYWSWIRQHPGKLEWIGYIYHSGNTYYNP 65

Qy  62  KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDGYT--LDIWGQGLTVTVSS 114
Db  66  KSRVITISVDTSKNQFSLKSLSVTAADTAVYYCAR--DGINYWFPLMGRGLTVTVSS 120

RESULT 10
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

```





```
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-19

Query Match      83.5%; Score 508.5; DB 15; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.1e-40;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

Qy 2 ESGFGLVKPAQTLSLSCAVSGGSIKSGGYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 6 ESGFGLVKPQTLSLTCTVSGGSIKSGGYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 65
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 KSRVTSVDTSENKQSLNSVTAAADTAVYYCAR-----LDGYTLIDWGQGLTVTVSS 114
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 66 KSRVTSVDTSENKQSLNSVTAAADTAVYYCARVTDYVYYGLDVGQGLTVTVSS 123
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 15
US-10-309-762-8
; Sequence 8, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-8

Query Match      83.5%; Score 508.5; DB 15; Length 125;
Best Local Similarity 79.2%; Pred. No. 1.1e-40;
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;

Qy 2 ESGFGLVKPAQTLSLSCAVSGGSIKSGGYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 6 ESGFGLVKPQTLSLTCTVSGGSIKSGGYSWIRQHPGKLEWIGYIYHSGNTYYNPSL 65
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 KSRVTSVDTSENKQSLNSVTAAADTAVYYCAR-----LDGY--TLIDWGQGLTVTVSS 114
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 66 KSRVTSVDTSENKQSLNSVTAAADTAVYYCARTYDILTGYPDADFDWGQGLTVTVSS 125
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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Search completed: August 8, 2004, 12:43:20  
Job time : 39.5182 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-7  
Perfect score: 609  
Sequence: 1 LESGPGVLVKAQTLISLCAV.....RLDGYTLDWGQTLVTYSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499	81.9	473	US-09-049-672A-4	Sequence 4, Appli
2	496	81.4	172	US-09-472-087-7	Sequence 7, Appli
3	496	81.4	172	US-09-472-087-86	Sequence 86, Appli
4	482	79.1	487	US-09-800-729-145	Sequence 145, App
5	471.5	77.4	119	US-08-360-125-5	Sequence 5, Appli
6	471.5	77.4	119	US-08-450-578-5	Sequence 5, Appli
7	471.5	77.4	119	US-09-017-628-5	Sequence 5, Appli
8	471.5	77.4	119	US-09-014-880-5	Sequence 5, Appli
9	471.5	77.4	119	US-09-025-769B-39	Sequence 39, Appli
10	471.5	77.4	119	US-09-025-769B-65	Sequence 65, Appli
11	471.5	77.4	119	US-08-450-363-5	Sequence 5, Appli
12	466	76.5	122	US-08-360-125-11	Sequence 11, Appli
13	466	76.5	122	US-08-450-578-11	Sequence 11, Appli
14	466	76.5	122	US-09-017-628-11	Sequence 11, Appli
15	466	76.5	122	US-09-014-880-11	Sequence 11, Appli
16	466	76.5	122	US-08-450-363-11	Sequence 11, Appli
17	455	74.7	118	US-09-025-769B-25	Sequence 25, Appli
18	453	74.4	118	US-08-545-809A-116	Sequence 116, App
19	446.5	73.3	250	US-10-039-785-50	Sequence 50, Appli
20	445	73.1	244	US-08-918-148-79	Sequence 79, Appli
21	442.5	72.7	142	US-08-480-774A-2	Sequence 2, Appli
22	438	71.9	278	US-09-260-527-3	Sequence 3, Appli
23	429.5	70.5	119	US-09-652-816A-10	Sequence 10, Appli
24	429	70.4	150	US-09-582-337-14	Sequence 14, Appli
25	427	70.1	118	US-09-343-698-6	Sequence 6, Appli
26	427	70.1	118	US-08-325-955-6	Sequence 6, Appli
27	425.5	69.9	476	US-08-487-550-12	Sequence 12, Appli

28	425.5	69.9	476	4	US-09-526-098-12	Sequence 12, Appli
29	424	69.6	118	3	US-08-545-809A-142	Sequence 142, App
30	422.5	69.4	98	1	US-08-478-039-75	Sequence 75, Appli
31	422.5	69.4	98	1	US-08-476-349A-75	Sequence 75, Appli
32	422	69.3	126	1	US-08-276-852-142	Sequence 142, App
33	422	69.3	126	1	US-08-899-575-142	Sequence 142, App
34	422	69.3	126	1	US-08-899-575-142	Sequence 142, App
35	422	69.3	126	5	PT-US95-08743-142	Sequence 142, App
36	420.5	69.0	124	1	US-08-478-039-78	Sequence 78, Appli
37	420.5	69.0	124	1	US-08-476-349A-78	Sequence 78, Appli
38	420	69.0	832	3	US-08-630-820-7	Sequence 7, Appli
39	420	69.0	832	4	US-09-273-453-7	Sequence 7, Appli
40	419.5	68.9	219	4	US-09-460-384-37	Sequence 37, Appli
41	418.5	68.7	96	3	US-08-851-362D-27	Sequence 27, Appli
42	418.5	68.7	117	3	US-08-851-362D-44	Sequence 44, Appli
43	418.5	68.7	123	4	US-08-793-450-4	Sequence 4, Appli
44	418.5	68.7	472	4	US-08-793-450-8	Sequence 8, Appli
45	418	68.6	244	4	US-10-039-785-44	Sequence 44, Appli

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANTUT01

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; CLONE: 1513264
US-09-049-672A-4

Query Match      81.9%; Score 499; DB 3; Length 473;
Best Local Similarity 78.2%; Pred. No. 3.6e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY 2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
DB 25  ESGPGLVKPSETLSLTCAVSGGSITSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 84
QY 62  KSRIAMSVDTSENKFSRLNSVTAAADTAVYYCARLDG-----GYTLDIWGQGLTVTVSS 114
DB 85  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDDVGLRGNGYGDVWGQGLTVTVSS 143

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      81.4%; Score 496; DB 4; Length 172;
Best Local Similarity 79.8%; Pred. No. 2.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 3  SGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 62
DB 1  SGPGLVKPQILSLTCTVSGGSISGGHYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 60
QY 63  SRIAMSVDTSENKFSRLNSVTAAADTAVYYCARLDG--YTLDIWGQGLTVTVSS 114
DB 61  SRVTISVDTSKNQFSLKLSVTAADTAVYYCARDSGDYIGIDVWGQGLTVTVSS 114

RESULT 4
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

Query Match      79.1%; Score 482; DB 4; Length 487;
Best Local Similarity 74.8%; Pred. No. 2e-41;
Matches 92; Conservative 12; Mismatches 9; Indels 10; Gaps 2;

QY 2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
DB 25  ESGPGLVKPSETLSLTCTVSGGSISGGHYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 84
QY 62  KSRIAMSVDTSENKFSRLNSVTAAADTAVYYCAR-----LDGYTL-----DIWGQGLTVT 111
DB 85  KSRVTISVDTSONQFSLRLSSVTAAADTAVYYCAKDHREATDGYQLEYRGFDYWGQGLTVT 144

RESULT 5
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
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; CLONE: 1513264
US-09-049-672A-4

Query Match      81.9%; Score 499; DB 3; Length 473;
Best Local Similarity 78.2%; Pred. No. 3.6e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY 2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
DB 25  ESGPGLVKPSETLSLTCAVSGGSITSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 84
QY 62  KSRIAMSVDTSENKFSRLNSVTAAADTAVYYCARLDG-----GYTLDIWGQGLTVTVSS 114
DB 85  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDDVGLRGNGYGDVWGQGLTVTVSS 143

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      81.4%; Score 496; DB 4; Length 172;
Best Local Similarity 79.8%; Pred. No. 2.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 3  SGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 62
DB 1  SGPGLVKPQILSLTCTVSGGSISGGHYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 60
QY 63  SRIAMSVDTSENKFSRLNSVTAAADTAVYYCARLDG--YTLDIWGQGLTVTVSS 114
DB 61  SRVTISVDTSKNQFSLKLSVTAADTAVYYCARDSGDYIGIDVWGQGLTVTVSS 114

RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
```

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:

PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-5  
Query Match 77.4%; Score 471.5; DB 1; Length 119;  
Best Local Similarity 75.9%; Pred. No. 4.6e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
Qy 2 ESGGLVKPQATLSLSCAVSGGSIIRSGGYWSWIRQHPGKLEWIGYIHSGNTYINPSL 61  
Db 6 ESGPGLVKPQATLSLCTVSGGSISSCGFYNNWIRQHPGKLEWIGYIYSGSYINPSL 65  
Qy 62 KSRIVMSVDTSSENKFSRLNSVTAAADTAVYCA---RLDGYTLDIWGQGLIVTVSS 114  
Db 66 KSRVTISLDTSKSQFSLKSLTAADTAVYCAKSTELRG--ADYWGQGTMTVTSS 119  
RESULT 6  
US-08-450-578-5  
Sequence 5, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:

STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 4.6e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIHSGNTYVNSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSISSCGFYWNIRQHPGKLEWIGYIYSGSTYVNSL 65  
QY 62 KSRVTSIDTSKQFSLKSLTAADTAVYICARSTRLEG--ADYWGQGTMTVSS 114  
DB 66 KSRVTSIDTSKQFSLKSLTAADTAVYICARSTRLEG--ADYWGQGTMTVSS 119

## RESULT 7

US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287ihiko  
APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
FILE REFERENCE: 177/527361KH  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 4.6e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIHSGNTYVNSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSISSCGFYWNIRQHPGKLEWIGYIYSGSTYVNSL 65  
QY 62 KSRVTSIDTSKQFSLKSLTAADTAVYICARSTRLEG--ADYWGQGTMTVSS 114  
DB 66 KSRVTSIDTSKQFSLKSLTAADTAVYICARSTRLEG--ADYWGQGTMTVSS 119

## RESULT 8

US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014.880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 75.9%; Pred. No. 4.6e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYVWSWIRQHPGKLEWIGYIHSGNTYNNPSL 61  
Db 6 ESGPGLVKPSETLSLCTVSGGSISSCGFYWNIRQHPGKLEWIGYIYSGSTYNNPSL 65  
Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVVYCA---RLDGYTLDIWGQGLTVTVSS 114  
Db 66 KSRVTISLDTSKSQFSLKSLSTAADTAVVYCARSTLRG--ADYWGQGLTVTVSS 119

## RESULT 9

US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9000

INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 77.6%; Pred. No. 4.6e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYVWSWIRQHPGKLEWIGYIHSGNTYNNPSL 61  
Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQHPGKLEWIGYIYSGSTYNNPSL 63  
Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG---YTLDIWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKSLSSVTAADTAVVYCARWGSGDFYAMDYWGQGLTVTVSS 119

## RESULT 10

US-09-025-769B-65  
; Sequence 65, Application US/09025769B  
; Patent No. 6300064

GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 77.6%; Pred. No. 4.6e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYVWSWIRQHPGKLEWIGYIHSGNTYNNPSL 61  
Db 6 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQHPGKLEWIGYIYSGSTYNNPSL 63  
Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG---YTLDIWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKSLSSVTAADTAVVYCARWGSGDFYAMDYWGQGLTVTVSS 119

## RESULT 11

US-08-450-363-5  
; Sequence 5, Application US/08450363  
; Patent No. 6436434  
; GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 6436434hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: May 25, 1995  
CLASIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 77.4%; Score 471.5; DB 4; Length 119;  
Best Local Similarity 75.9%; Pred. No. 4.6e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;  
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYKSWIRQHPGKGLWIGYIYHSGNTYYNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSISSCGFGYWNWIRQHPGKGLWIGYIYSGSTYYNPSL 65  
QY 62 KSRIAMSVDTSENKFSRLNSVTRADTAVYYCA---RLDGYTLDIWGQGLTVTVSS 114  
DB 66 KSRVTISLDTSKQSFSLKSLTRADTAVYYCAKSTRLRG--ADYWGQGLTVTVSS 119  
RESULT 12  
US-08-360-125-11  
Sequence 11, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:



CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match 76.5%; Score 466; DB 1; Length 122;  
Best Local Similarity 75.2%; Pred. No. 1.7e-40;  
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPLVKPAQTLSLSCAVSGGSRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61  
Db 6 ESGPLVKPSETLSLCTVSGGSISSSYWGIRQPPGKLEWIGSYSGTYINPSL 65  
QY 62 KSRIAMSVDTSENKFSRLNSVTAAATAVYICAR--LDG--YTLDIWGGTTLTVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARSGYGGYGMVWVGQTTTVSS 122

## RESULT 13

US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845

## GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match 76.5%; Score 466; DB 2; Length 122;  
Best Local Similarity 75.2%; Pred. No. 1.7e-40;  
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPLVKPAQTLSLSCAVSGGSRSGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61  
Db 6 ESGPLVKPSETLSLCTVSGGSISSSYWGIRQPPGKLEWIGSYSGTYINPSL 65  
QY 62 KSRIAMSVDTSENKFSRLNSVTAAATAVYICAR--LDG--YTLDIWGGTTLTVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARSGYGGYGMVWVGQTTTVSS 122

## RESULT 14

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US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match          76.5%; Score 466; DB 2; Length 122;
Best Local Similarity 75.2%; Pred. No. 1.7e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPLVKPAQTLSLSCAVSGGSIKSGGYWIRQHPGKLEWIGYIYHSGNTYINPSSL 61
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Db 6 ESGPLVKPSETLSLTCTVSGGSISSSYWGWIRQPPGKLEWIGSIYSGTYINPSSL 65
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 KSRITMSVDTSENKFSRLNSVTAADTAVYICAR--LDG--YTLDIWGGGTLVTVSS 114
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Db 66 KSRVTISVDTSKNQPSLSSVTAADTAVYICARGSYGGYYGMDVWVGQGITVTVSS 122
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RESULT 15
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
```

```
ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

Query Match          76.5%; Score 466; DB 2; Length 122;
Best Local Similarity 75.2%; Pred. No. 1.7e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPLVKPAQTLSLSCAVSGGSIKSGGYWIRQHPGKLEWIGYIYHSGNTYINPSSL 61
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 6 ESGPLVKPSETLSLTCTVSGGSISSSYWGWIRQPPGKLEWIGSIYSGTYINPSSL 65
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 KSRITMSVDTSENKFSRLNSVTAADTAVYICAR--LDG--YTLDIWGGGTLVTVSS 114
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 66 KSRVTISVDTSKNQPSLSSVTAADTAVYICARGSYGGYYGMDVWVGQGITVTVSS 122
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Search completed: August 8, 2004, 12:20:23
Job time : 14.6455 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 10.0182 Seconds  
(without alignments)  
1094.593 Million cell updates/sec

Title: US-10-027-725A-8  
Perfect score: 614  
Sequence: 1 LESGPLVKPSQTSLTCTV.....RSDGVTLDNMGQGLVTIVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain v r
3	487	79.3	130	2 S30534	Ig heavy chain v r
4	480.5	78.3	121	2 S44113	Ig heavy chain v r
5	478.5	77.9	140	2 I37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain v r
7	474.5	77.3	116	2 S37456	Ig mu chain huma
8	474.5	77.3	130	2 S31690	Ig heavy chain v r
9	474	77.2	122	2 S69912	Ig V-D-J region
10	473.5	77.1	128	2 S31514	Ig heavy chain - h
11	472.5	77.0	127	2 S19668	Ig heavy chain v r
12	469	76.4	137	2 S31676	Ig heavy chain v r
13	468.5	76.3	123	2 S30530	Ig heavy chain v r
14	465.5	75.8	155	2 S31511	Ig heavy chain v r
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.2	139	2 S31586	Ig heavy chain v r
17	460.5	75.0	146	2 S09711	Ig heavy chain v r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain v r
20	457	74.4	110	2 S44110	Ig heavy chain v r
21	455	74.1	99	2 S26803	Ig heavy chain v r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain v r
24	452	73.6	129	2 S44114	Ig heavy chain v r
25	450	73.3	99	2 S26802	Ig heavy chain v r
26	450	73.3	135	2 S31604	Ig heavy chain v r
27	447	72.8	118	2 S20780	Ig heavy chain v r
28	446	72.6	99	2 S12418	Ig heavy chain v r
29	444.5	72.4	139	2 S31696	Ig heavy chain v r

## ALIGNMENTS

## RESULT 1

S78051

Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999

C:Accession: S78051; S23716

R:Harindranath, N.

submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78051

A:Molecule type: mRNA

A:Residues: 1-135 <HAR>

A:Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117

R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins

Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity B cell receptors

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23716

A:Molecule type: mRNA

A:Residues: 13-111 <HAW>

A:Cross-references: EMBL:X54437

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 499.5; DB 2; Length 135;

Best Local Similarity 79.7%; Pred. No. 9.3e-38;

Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTSLTCTVSGGSIKSGYVMSVROPPGKGLWIGNIYSGTYNPSL 61

Db 18 ESGPGLVKPSQTSLTCTVSGGSIKSGYVMSVROPPGKGLWIGNIYSGTYNPSL 77

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTVVYCAR--SDGYTLDN--WGQGLVTIVSS 114

Db 78 KSRITMSVDTSKNHFSLRLTSVTAADTVVYCARLGPDDYTLDMVWGQGLVTIVSS 135

## RESULT 2

S13519

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S13519

R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A:Reference number: S13519; MUID:91187691; PMID:2011536

A:Accession: S13519

```
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match      80.7%; Score 495.5; DB 2; Length 147;
Best Local Similarity 80.2%; Pred. No. 2.3e-37;
Matches 93; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

Qy 2 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61
Db 32 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 91

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSDG---DGYTLDNWGQGLTVTVSS 114
Db 92 KSRVTSVDTSKNQFSLKLSVTAADTAVYCARLLWFGELFDYWGQGLTVTVSS 147

RESULT 3
S30534
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
R:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAR>
A:Cross-references: EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match      79.3%; Score 487; DB 2; Length 130;
Best Local Similarity 76.0%; Pred. No. 1.2e-36;
Matches 95; Conservative 7; Mismatches 11; Indels 12; Gaps 2;

Qy 2 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61
Db 6 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSDG-----YT-----LDNWGQGLT 109
Db 66 KSRVTSVDTSKNQFSLKLSVTAADTAVYCARDKGFGWSGYITNSRAAFDIWQGT 125

Qy 110 VTVSS 114
Db 126 VTVSS 130

RESULT 4
S44113
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
R:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S44113
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAW>
A:Cross-references: EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:g940524
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

F:15-99/Domain: immunoglobulin homology <IMM>

```
Query Match      78.3%; Score 480.5; DB 2; Length 121;
Best Local Similarity 78.4%; Pred. No. 4.1e-36;
Matches 91; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 2 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61
Db 6 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSDGY--TLDNWGQGLTVTVSS 114
Db 66 KSRVTSVDTSKNQFSLKLSVTAADTGVYCSRLSGGYSDFDYWGQGLTVTVSS 121
```

#### RESULT 5

Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
R:Accession: I37782; S25476  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37782  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IMM>

```
Query Match      77.9%; Score 478.5; DB 2; Length 140;
Best Local Similarity 78.8%; Pred. No. 7.2e-36;
Matches 93; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

Qy 2 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61
Db 25 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 82

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSD-----CYTLDNWGQGLTVTVSS 114
Db 83 KSRVTSVDTSKNQFSLKLSVTAADTAVYCARHNSWSWYGRYFDYWGQGLTVTVSS 140
```

#### RESULT 6

Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
R:Accession: S09710  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains  
A:Reference number: S09710; MUID:90262535; PMID:2111699  
A:Accession: S09710  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <HUG>  
A:Cross-references: EMBL:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

```
Query Match      77.8%; Score 477.5; DB 2; Length 146;
Best Local Similarity 73.2%; Pred. No. 9.3e-36;
Matches 90; Conservative 13; Mismatches 9; Indels 11; Gaps 2;

Qy 2 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61
Db 25 ESGPLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 84
```



C;Accession: S19668; S24445  
R;Marks: J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 561-597, 1991  
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage particles.  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19668  
A;Molecule type: mRNA  
A;Residues: 1-127 <MAR>  
A;Cross-references: EMBL:X61648  
R;Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A;Reference number: S24442  
A;Accession: S24445  
A;Molecule type: mRNA  
A;Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F' <JON>  
A;Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;  
Best Local Similarity 73.0%; Pred. No. 2.2e-35;  
Matches 89; Conservative 12; Mismatches 12; Indels 9; Gaps 1;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYINPSL 61  
DB 6 QSGGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGSVHSGPTIYNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 112  
DB 66 KSRVTMSVDTSKNQPSLKLKSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 125

QY 113 SS 114  
DB 126 SS 127

RESULT 12  
S31676  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31676  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31676  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-137 <CUI>  
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 137;  
Best Local Similarity 80.0%; Pred. No. 5e-35;  
Matches 92; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYINPSL 61  
DB 25 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGRIYTGSTYINPSL 82

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 114  
DB 83 KSRVTMSVDTSKNQPSLKLKSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 137

RESULT 13  
S30530  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S30530  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30530  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-123 <MAR>  
A;Cross-references: EMBL:Z18316  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 468.5; DB 2; Length 123;  
Best Local Similarity 75.6%; Pred. No. 4.9e-35;  
Matches 90; Conservative 11; Mismatches 11; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYINPSL 61  
DB 6 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGSVHSGPTIYNPSL 64

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----SDGYTLDNWGGTTLTVV 114  
DB 65 KSRVTISVDTSKNQPSLKLKSVTAADTAIVYCARSDG-----SDGYTLDNWGGTTLTVV 123

## RESULT 14

S31511

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31511

R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au

A;Reference number: S31509

A;Accession: S31511

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 &lt;CHA&gt;

A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-129/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 75.8%; Score 465.5; DB 2; Length 155;

Matches 89; Conservative 11; Mismatches 11; Indels 9; Gaps 2;

QY

2 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYINPSL 61

DB 38 ESGPGLVKPSTLSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGRIYTGSTYINPPL 95

QY

62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 114

DB 96 KSRVTISVDTSKNQPSLKLKSVTAADTAIVYCARSDG-----YTLDNWGGTTLTVV 155

## RESULT 15

S31512

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31512

R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA au

A;Reference number: S31509

A;Accession: S31512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 &lt;CHA&gt;

A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA494.1; PID:g33083  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

```
Query Match      75.5%; Score 463.5; DB 2; Length 155;
Best Local Similarity 73.3%; Pred. No. 1.8e-34;
Matches 88; Conservative 12; Mismatches 11; Indels 9; Gaps 2;

QY  2  ESGPGLVKPSQTLSTCTVSGGSIIRSGGYYSWVPPKGLWIGNIYHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  38  ESGPGLVFPSELSTCTVSGGSISS--YYSWIRQPPKGLWIGIYITGSAIYNPPI 95
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  96  KSRVTISVDTSKNQFSLKVSSTAADTAVYYCARGGGISSWVYVYGMVDVWGQGLVTVSS 155
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: August 8, 2004, 12:18:54  
Job time : 11.0182 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 6.21818 Seconds  
(without alignments)  
954.620 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LESGFLVKPSQILSLTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	440.5	71.7	129	1	HV2F_HUMAN
2	417	67.9	146	1	HV2I_HUMAN
3	381.5	62.1	117	1	HV2G_HUMAN
4	363.5	59.2	137	1	HV46_MOUSE
5	352.5	57.4	144	1	HV43_MOUSE
6	347.5	56.6	113	1	HV47_MOUSE
7	338.5	55.1	116	1	HV61_MOUSE
8	335	54.6	117	1	HV62_MOUSE
9	332.5	54.2	116	1	HV60_MOUSE
10	325	52.9	135	1	HV02_XENLA
11	314	51.1	120	1	HV2B_HUMAN
12	295.5	48.1	119	1	HV2C_HUMAN
13	294	47.9	147	1	HV2H_HUMAN
14	288.5	47.0	136	1	HV01_XENLA
15	288	46.9	115	1	HV44_MOUSE
16	288	46.9	119	1	HV40_MOUSE
17	287.5	46.8	125	1	HV2D_HUMAN
18	286.5	46.7	121	1	HV2E_HUMAN
19	285.5	46.5	117	1	HV2B_RABIT
20	283	46.1	126	1	HV2A_HUMAN
21	282	45.9	114	1	HV3B_HUMAN
22	281	45.8	122	1	HV3A_HUMAN
23	281	45.8	122	1	HV3G_HUMAN
24	278	45.3	119	1	HV37_MOUSE
25	277	45.1	116	1	HV05_CARAU
26	276.5	45.0	121	1	HV3J_HUMAN
27	276	45.0	119	1	HV38_MOUSE
28	275	44.8	116	1	HV45_MOUSE
29	274.5	44.7	142	1	HV01_RAT
30	274	44.6	136	1	HV2C_RABIT
31	273.5	44.5	117	1	HV41_MOUSE
32	273.5	44.5	117	1	HV42_MOUSE
33	272	44.3	114	1	HV2A_RABIT

34	271	44.1	122	1	HV3H_HUMAN	P01769 homo sapien
35	267	43.5	118	1	HV51_MOUSE	P06330 mus musculus
36	267	43.5	139	1	HV07_MOUSE	P01751 mus musculus
37	265.5	43.2	117	1	HV12_MOUSE	P01756 mus musculus
38	264.5	43.1	115	1	HV3D_HUMAN	P01765 homo sapien
39	264.5	43.1	117	1	HV13_MOUSE	P01757 mus musculus
40	264	43.0	122	1	HV20_MOUSE	P01789 mus musculus
41	262.5	42.8	115	1	HV3F_HUMAN	P01787 homo sapien
42	262.5	42.8	117	1	HV02_CANFA	P01785 canis famil
43	261	42.5	116	1	HV3T_HUMAN	P01781 homo sapien
44	261	42.5	126	1	HV3K_HUMAN	P01772 homo sapien
45	260	42.3	120	1	HV50_MOUSE	P06329 mus musculus

## ALIGNMENTS

RESULT 1  
HV2F\_HUMAN  
ID HV2F\_HUMAN STANDARD; PRT; 129 AA.  
AC P01824;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-l region WAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=82222235; PubMed=6806818;  
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02099; D2HUMA.  
DR HSPP; P01825; 7FAB.  
DR GlycoSuiteDB; P01824; -  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 113 IG-LIKE.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;  
Best Local Similarity 65.1%; Pred. No. 1.7e-38;  
Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;  
QY 2 ESGPGLVKPSQILSLTCTVSGGSIRSGGYWSVRQPPGKGLWIGNIVHSGNTYNPSL 61  
Db 6 ESGPGLVKPSQILSLTCTVSGGSIRSGGYWSVRQPPGKGLWIGNIVHSGNTYNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTAAATVAVYCAR-----SDGYTLDNWGQGT 108  
Db 66 RGRVITSVDTSRNQFSNLRLSRMSADTANYCARGNPPPYDYGTSDDG--IDWVGQGT 123  
QY 109 LTVVSS 114  
Db 124 TVHVSS 129  
RESULT 2

QY	2	ESGPGLVKPQSLTCTVSGGSI	RSQGYWSVRQPPGKLEWIGNIYHSGNTYINPSL	61
Db	6	QSGPGLVKPQSLTCTVSGGSI	RSQGYWSVRQPPGKLEWIGNIYHSGNTYINPSL	63
QY	62	KSRITMSVDTSKNHFSLRLTSVTAADTAVYICARS-	DGYTLDNWQGLTVTVSS	114
Db	64	RSRVTLVDTSKNQFSLRLSSVTAADTAVYICARNLIAGCIDVWGQGLTVTVSS		117
RESULT 4				
HV46_MOUSE				
ID	HV46_MOUSE	STANDARD;	PRT;	137 AA.
AC	P01822;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig heavy chain V region MOPC 315 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

QY	4	GPGLVKPQSLTCTVSGGSI	RSQGYWSVRQPPGKLEWIGNIYHSGNTYINPSLKS	63
Db	28	GAGLVKPESETLSLTCAPVFGSP--	SGYWSWISQPPGRLGWTGENHSGSNYKTSLSKS	85
QY	64	RITMSVDTSKNHFSLRLTSVTAADTAVYICARS---	DG-----YTLDNWQGLTVTVS	113
Db	86	RVTISLDTSKNLFSLKLSVTAADTAVYICARGLLRGGWVDVYYYGMDVWGQGTITVTS		145
QY	114	S 114		
Db	146	S 146		
RESULT 3				
HV2G_HUMAN				
ID	P01825;	STANDARD;	PRT;	117 AA.
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V-II region NEMM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE..77242302; PubMed=407927;			
RX	MEDLINE=77242302; PubMed=407927;			
RA	Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;			
RT	"Amino acid sequence of the VH region of a human myeloma			
RT	immunoglobulin (IgG New).";			

Biochemistry 16:3412-3420(1977) .				
[2]				
RN	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.			
RX	MEDLINE=78066916; PubMed=618887;			
RA	Saul P.A., Amzel L.M., Poljak R.J.;			
RT	"Preliminary refinement and structural analysis of the Fab fragment			
RT	from human immunoglobulin new at 2.0-A resolution.";			
RL	J. Biol. Chem. 253:585-597(1978).			
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA			
CC	PROTEIN.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A90404; G1HUNM.			
DR	PDB; 7FAB; 31-JAN-94.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.			
FT	DOMAIN	1	111	IG-LIKE.
FT	MOD RES	1	1	PYRROLIDONE CARBOXYLIC ACID.
FT	STRAND	3	7	
FT	STRAND	11	12	
FT	TURN	14	15	
FT	STRAND	18	25	
FT	TURN	30	31	
FT	STRAND	33	39	
FT	TURN	41	42	
FT	STRAND	46	51	
FT	TURN	53	54	
FT	STRAND	57	59	
FT	HELIX	61	63	
FT	TURN	64	66	
FT	STRAND	67	72	
FT	TURN	73	76	
FT	STRAND	77	82	
FT	HELIX	87	89	
FT	STRAND	91	98	
FT	STRAND	104	107	
FT	STRAND	111	115	
FT	NON TER	117	117	
SQ	SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;			
Query Match 62.1%; Score 381.5; DB 1; Length 117;				
Best Local Similarity 65.8%; Pred. No. 1.8e-32;				
Matches 75; Conservative 17; Mismatches 19; Indels 3; Gaps 2;				



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RESULT 6
HV47 MOUSE STANDARD; PRT; 113 AA.
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=84024551; PubMed=6414509;
RA Juszczak E.C., Margolies M.N.;
RT "Amino acid sequence of the heavy chain variable region from the A/J
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
RT idio type."
RL Biochemistry 22:4291-4296(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
CC STRAIN A/J MICE.
DR PIR; A02098; G2MS60.
DR PDB; 1J10; 18-FEB-03.
DR PDB; 1J1P; 18-FEB-03.
DR PDB; 1J1X; 18-FEB-03.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

Query Match 56.6%; Score 347.5; DB 1; Length 113;
Best Local Similarity 61.9%; Pred. No. 5.5e-29;
Matches 70; Conservative 15; Mismatches 23; Indels 5; Gaps 2;

QY 2 ESGPLVKPSQTLSTCTVSGSIRSGGYVSWVRQPPCKGLEWIGNIYHSGNTYNPSL 61
DB 6 ESGPLVKPSQTLSTCTVSGSIRSGGYVSWVRQPPCKGLEWIGNIYHSGNTYNPSL 63

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVSS 114
DB 64 KSRISITRSTKNQYQLNSVTSEDTATYYCT---SLRFAYWGQGLTVSA 113

RESULT 7
HV61 MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; JT0510; HVMS73.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 1595517827F9768E CRC64;

Query Match 54.6%; Score 335; DB 1; Length 117;
Best Local Similarity 67.0%; Pred. No. 1.1e-27;
Matches 63; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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DR PIR; JT0508; HVMS1B.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 55.1%; Score 338.5; DB 1; Length 116;
Best Local Similarity 70.2%; Pred. No. 4.8e-28;
Matches 66; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 2 ESGPLVKPSQTLSTCTVSGSIRSGGYVSWVRQPPCKGLEWIGNIYHSGNTYNPSL 61
DB 24 ESGPLVKPSQSLSTCTVTGYSITS-GYSWHIRQPFQKLEWNGYIHYSGNTSYNP 82

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYICAR 95
DB 83 KSRISITRSTKNQFLQLNSVTEDTATYYCAR 116

RESULT 8
HV62 MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 733 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; JT0510; HVMS73.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 1595517827F9768E CRC64;

Query Match 54.6%; Score 335; DB 1; Length 117;
Best Local Similarity 67.0%; Pred. No. 1.1e-27;
Matches 63; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWVRQPPGKGLVIGTNIYHSGNTYNPSL 61
Db 24 ESGPGLVKPSQIALTCTVTGSIITGNVRSWKIRQFPNGKLEWIGYISAITSYNPSP 83

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
Db 84 KSRITITRDTSKNQFFLENNLSITAEDETATYYCAR 117

RESULT 9
HV00 MOUSE
ID HV00 MOUSE STANDARD; PRT; 116 AA.
AC F18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/GJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
DR PIR; J05059; HVMS31.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03B53DC9E10 CRC64;

Query Match 54.2%; Score 332.5; DB 1; Length 116;
Best Local Similarity 67.0%; Pred. No. 2e-27;
Matches 63; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWVRQPPGKGLVIGTNIYHSGNTYNPSL 61
Db 24 ESGPGLVKPSQIALTCTVSGTSGYISITS-GYYNNIRQPPGKLEWIGYISYDGSNNYNPSL 82

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
Db 83 KNRISITRDTSKNQFFLENNLSITAEDETATYYCAR 116

RESULT 10
HV02 XENLA
ID HV02 XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

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OX NCBI_TaxID=9355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1 18
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 52.9%; Score 325; DB 1; Length 135;
Best Local Similarity 54.8%; Pred. No. 1.4e-26;
Matches 63; Conservative 17; Mismatches 31; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWVRQPPGKGLVIGTNIYHSGNTYNPSL 61
Db 23 ESGPGLVKPSQIALTCTVSGFELSS--YHWHIRQPPGKLEWIGYIATGGSTAIADSL 80

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGYTLNWSGGTLVTSS 114
Db 81 KNRVITIKDNGKKQVYLQMGMEVKDTAMYICAREYASGYNFDYWGQGTWVTVTS 135

RESULT 11
HV2B HUMAN
ID HV2B HUMAN STANDARD; PRT; 120 AA.
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
heavy chains.";
RL Biochem. J. 117:641-660 (1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02089; GHUCCO.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.

```

DR GO: 0003823; F: antigen binding; NAS.  
 DR GO: 0006955; P: immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; IG; 1.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 110  
 FT MOD RES 1 1  
 FT DISULFID 22 94  
 FT CARBOHYD 62 62  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EB98 CRC64;  
 Query Match 51.1%; Score 314; DB 1; Length 120;  
 Best Local Similarity 55.5%; Pred. No. 1.7e-25;  
 Matches 66; Conservative 14; Mismatches 29; Indels 10; Gaps 3;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYVSWVRQPGKGLWIGNIYHSGNTYINPSL 61  
 DB 6 ESGPALVRPTQTLTCTCFSGLSSTGCVGWIRQPPGKGLWLRIDWDDDKYINTSL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCAR-----SDGYTLDNWGQGLTVTSS 114  
 DB 66 ETRLTISKDTSRNQVLIMDPV---DTATYICARITVIPAPAGY-MDVWGRGTPVTSS 120  
 RESULT 12  
 HV2C\_HUMAN  
 ID HV2C\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01816;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region DAW.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70258837; PubMed=5449120;  
 RA Press E.M., Hogg N.M.;  
 RT "The amino acid sequences of the Fd fragments of two human gamma-1  
 RT heavy chains."  
 RL Biochem. J. 117:641-660(1970).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE  
 CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02091; GIHWDW.  
 DR HSSP; P01789; 1MCP.  
 DR GO: 0005576; C: extracellular; NAS.  
 DR GO: 0003823; F: antigen binding; NAS.  
 DR GO: 0006955; P: immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 113  
 FT MOD RES 1 1  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;  
 Query Match 48.1%; Score 295.5; DB 1; Length 119;  
 Best Local Similarity 52.6%; Pred. No. 1.3e-23;  
 Matches 60; Conservative 16; Mismatches 37; Indels 1; Gaps 1;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYVSWVRQPGKGLWIGNIYHSGNTYINPSL 61  
 DB 6 ESGPALVRPTQTLTCTCFSGLSSTGCVGWIRQPPGKGLWLRIDWDDDKYIGASL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-YTLDNWGQGLTVTSS 114  
 DB 66 ETRLAVSKDTSKNQVLISMTVPGDGTATYVCARSGSQYFDYWGQGLTVTSS 119  
 RESULT 13  
 HV2H\_HUMAN  
 ID HV2H\_HUMAN STANDARD; PRT; 147 AA.  
 AC P04438;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region SESS precursor.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84298107; PubMed=6089186;  
 RA Takahashi N., Noma T., Honjo T.;  
 RT "Rearranged immunoglobulin heavy chain variable region (VH)  
 RT pseudogene that deletes the second complementarity-determining  
 RT region."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).  
 DR PIR; A02090; G2HUOS.  
 DR HSSP; P01825; 7FAB.  
 DR GO: 0005576; C: extracellular; NAS.  
 DR GO: 0003823; F: antigen binding; NAS.  
 DR GO: 0006955; P: immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 147  
 FT DOMAIN 20 118  
 FT DOMAIN 119 132  
 FT DOMAIN 133 147  
 FT NON\_TER 147 147  
 SQ SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB6666 CRC64;  
 Query Match 47.9%; Score 294; DB 1; Length 147;  
 Best Local Similarity 49.6%; Pred. No. 2.4e-23;  
 Matches 58; Conservative 15; Mismatches 34; Indels 10; Gaps 1;  
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYVSWVRQPGKGLWIGNIYHSGNTYINPSL 61  
 DB 25 ESGPALVKATHTLTCTCFSGLSVTRGMSVWIRQPPGKALEWLARIDWDDDKYGTSL 84  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSD-----GYTLDNWGQGT 108  
 DB 85 ETRLTISKDTSKNQVLKVTNMDPADTATYVCARMQVTWVRVMTSNADFVWQGT 141  
 RESULT 14  
 HV01\_XENLA  
 ID HV01\_XENLA STANDARD; PRT; 136 AA.  
 AC P20956;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region XIG8 precursor (Fragment).  
 OS Xenopus laevis (African clawed frog)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; M20484; AAA49774.1; ALT_TERM.
DR F1R; A31933; A31933.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW
FT NON TER 1
FT SIGNAL <1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT DOMAIN 19 128 IG-LIKE.
FT NON TER 136
FT SEQUENCE 136 AA; 15123 MW; 314183981441963 CRC64;
Query Match 47.0%; Score 288.5; DB 1; Length 136;
Best Local Similarity 50.4%; Pred. No. 8e-23;
Matches 59; Conservative 19; Mismatches 32; Indels 7; Gaps 3;
QY 2 ESGPGLVKPSQTLSLCTVSGGSIKSGYYSWVRPPGKGLWIGNIYHSGNTYNPSL 61
Db 23 ESGPGLVKPSQTLSLCTVSGGSIKSGYYSWVRPPGKGLWIGNIYHSGNTYNPSL 61
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYVC---ARSDGYTLDNWGQGLTVTVSS 114
Db 81 KNRVTITKNGKQVQLQNMGMVYKDTAMYCTSTLAGTAGY-FEHWGQGLTVTVTS 136
RESULT 15
HV44 MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC EMBL; V00767; CAA24148.1; -
DR F1R; A02095; HVMS14.
DR PDB; 1A7N; 29-APR-98.
DR PDB; 1A7O; 29-APR-98.
DR PDB; 1A7P; 29-APR-98.
DR PDB; 1A7R; 29-APR-98.
DR PDB; 1G7H; 17-JAN-01.
DR PDB; 1G7I; 17-JAN-01.
DR PDB; 1G7J; 17-JAN-01.
DR PDB; 1G7M; 17-JAN-01.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
KW
FT SIGNAL 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PU14.
FT DOMAIN 20 >115 IG-LIKE.
FT NON TER 115
FT SEQUENCE 115 AA; 12447 MW; 7569DD4A843D500 CRC64;
Query Match 46.9%; Score 288; DB 1; Length 115;
Best Local Similarity 60.2%; Pred. No. 7.5e-23;
Matches 56; Conservative 15; Mismatches 20; Indels 2; Gaps 1;
QY 2 ESGPGLVKPSQTLSLCTVSGGSIKSGYYSWVRPPGKGLWIGNIYHSGNTYNPSL 61
Db 25 ESGPGLVKPSQTLSLCTVSGGSIKSGYYSWVRPPGKGLWIGNIYHSGNTYNPSL 61
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYVC 94
Db 83 KSRITMSVDTSKNHFSLRTSVTAADTAVYVC 94
Search completed: August 8, 2004, 12:14:31
Job time : 6.21818 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	476.5	77.6	492	4	Q7Z374	Q7Z374 homo sapien
2	470	76.5	478	4	Q7Z379	Q7Z379 homo sapien
3	466	75.9	150	4	Q9S973	Q9S973 homo sapien
4	466	75.9	496	4	Q96KX8	Q96KX8 homo sapien
5	463.5	75.5	119	4	Q9UL73	Q9UL73 homo sapien
6	457	74.4	613	4	Q96EY0	Q96EY0 homo sapien
7	429	69.9	130	4	Q9I1ZD7	Q9I1ZD7 homo sapien
8	427	69.5	139	4	Q96SX2	Q96SX2 homo sapien
9	426.5	69.5	588	4	Q9WUX4	Q9WUX4 homo sapien
10	426.5	69.5	597	4	Q9BU10	Q9BU10 homo sapien
11	426.5	69.5	618	4	Q96AA6	Q96AA6 homo sapien
12	422.5	68.8	597	4	Q9QB88	Q9QB88 homo sapien
13	413	67.3	473	4	Q9TC63	Q9TC63 homo sapien
14	386	62.9	116	4	Q7Z3Y6	Q7Z3Y6 homo sapien
15	382.5	62.3	479	11	Q99W22	Q99W22 mus musculus
16	365	59.4	122	4	Q9UL75	Q9UL75 homo sapien

```
ID Q72379 PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN DKFZp686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 76.5%; Score 470; DB 4; Length 478;
Best Local Similarity 75.7%; Pred. NO. 9.3e-41;
Matches 87; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

QY 2 ESGGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLWIGNTYHSGNTYNPSSL 61
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 24 ESGGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLWIGNTYHSGNTYNPSSL 83
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRITMSYDTSKNHPSRLTSVTAAATAVYCARSDGY--TIDNWGQGLTVTVSS 114
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 84 ESRISISIDTSKNQPSRLNLSLTAAATAVYFCARGVGLGTAPDIWGQGLTVTVSS 138
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
O95973 PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IgM secreting B cell in the synovium of
RT Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSP; P01825; 7EAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT NON TER 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 4; Length 150;
Best Local Similarity 76.1%; Pred. NO. 5.8e-41;
Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 ESGGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLWIGNTYHSGNTYNPSSL 61
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420A0BE CRC64;

Query Match      75.5%; Score 463.5; DB 4; Length 119;
Best Local Similarity 77.6%; Pred. No. 7.9e-41;
Matches 90; Conservative 9; Mismatches 11; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPQSLTCTVSGGSIKSGYKSWVRQPGKLEWIGNIYHSGNTYINPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YVSWIRQPGKLEWIGNIYHSGNTYINPSL 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYICARSDG---YTLNMGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNMGPPYFDYWGQGLTVTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
Q96EYO PRELIMINARY; PRT; 613 AA.
AC Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421B7 CRC64;

Query Match      74.4%; Score 457; DB 4; Length 613;
Best Local Similarity 78.0%; Pred. No. 2.9e-39;
Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;

Qy 2 ESGPGLVKPQSLTCTVSGGSIKSGYKSWVRQPGKLEWIGNIYHSGNTYINPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 ESGPGLVKPSETLSLTCTVSGGSISS--YVSWIRQPGKLEWIGNIYHSGNTYINPSL 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYICARSDGYTLDN-----WGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 KSRVTISVDRSKNQFSLKLTSLTAADTAVYICARLSNMGPPYFDYWGQGLTVTVSS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
   Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match      69.8%; Score 429; DB 4; Length 130;
Best Local Similarity 68.8%; Pred. No. 3.6e-37;
Matches 86; Conservative 12; Mismatches 15; Indels 12; Gaps 4;

Qy 2 ESGPGLVKPQSLTCTVSGGSIKSGYKSWVRQPGKLEWIGNIYHSGNT-----Y 56
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 QSGPGLVKPSETLSLTCTVSGGSISSSYWGIQSPGKLEWIGSYSGSYSGSPY 65
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 57 YNPSLSKRITMSVDTSKNHFSLRTSVTAADTAVYICAR----SDG--YT-LDNWGQGL 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 YAFSLRSRVIISVDTSKNQSLRLSSVTAADTAVYICASPTHCSGGGCAFFQHWGQGL 125
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 110 VTVSS 114
   |||||
Db 126 VTVSS 130

RESULT 8
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)
   of Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX249300; CAD62627.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 139
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
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Query Match          69.5%; Score 427; DB 4; Length 139;
Best Local Similarity 85.1%; Pred. No. 6.4e-37;
Matches 80; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

Qy 2 ESGGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 38 ESGGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 95

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 96 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCAR 129

RESULT 9
Q8WUX4 PRELIMINARY; PRT; 588 AA.
ID Q8WUX4
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match          69.5%; Score 426.5; DB 4; Length 588;
Best Local Similarity 70.0%; Pred. No. 4.3e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 GAGLLKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 84

Qy 64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDG-YTLDNWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 RVTISVDTSKKQLSKLSSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 10
Q9BU10 PRELIMINARY; PRT; 597 AA.
ID Q9BU10
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.

Query Match          69.5%; Score 427; DB 4; Length 139;
Best Local Similarity 85.1%; Pred. No. 6.4e-37;
Matches 80; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

Qy 2 ESGGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 38 ESGGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 95

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 96 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYYCAR 129

RESULT 9
Q8WUX4 PRELIMINARY; PRT; 588 AA.
ID Q8WUX4
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match          69.5%; Score 426.5; DB 4; Length 588;
Best Local Similarity 70.0%; Pred. No. 4.3e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 GAGLLKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 84

Qy 64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDG-YTLDNWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 RVTISVDTSKKQLSKLSSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 10
Q9BU10 PRELIMINARY; PRT; 597 AA.
ID Q9BU10
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.
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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAFB7E055851 CRC64;

Query Match          69.5%; Score 426.5; DB 4; Length 597;
Best Local Similarity 70.0%; Pred. No. 4.4e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 GAGLLKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 84

Qy 64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDG-YTLDNWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 RVTISVDTSKKQLSKLSSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 11
Q96AA6 PRELIMINARY; PRT; 618 AA.
ID Q96AA6
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96BDD4C7C696E0A6 CRC64;

Query Match          69.5%; Score 426.5; DB 4; Length 618;
Best Local Similarity 70.0%; Pred. No. 4.6e-36;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGLVKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 GAGLLKPSQTLTCTVSGGSIKSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSSL 84

Qy 64 RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDG-YTLDNWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 RVTISVDTSKKQLSKLSSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 12
Q9BQB8 PRELIMINARY; PRT; 597 AA.
ID Q9BQB8
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
```



```
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match      62.3%; Score 382.5; DB 11; Length 479;
Best Local Similarity 66.7%; Pred. No. 1.4e-31;
Matches 76; Conservative 15; Mismatches 20; Indels 3; Gaps 3;

Qy      2  ESGPGLVKPSQTLSLTCTVSGSIRSGGYKSWVRQPPGKGLWIGNIYHSGNTYYNP 61
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      24  ESGPGLVKPSQSLSLTCSVTGYSITS-GYYWNWIRQFPGNKLEWNGYINIDGSNNYNP 82
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy      62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGTFLTVSS 114
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      83  KNRISITFDTSKNQFFLKLNSVTTEDTATYYCA-SRGYSWFPNMGQGTFLTVSA 135
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Search completed: August 8, 2004, 12:17:44  
Job time : 31.2636 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds  
(without alignments)  
688.123 Million cell updates/sec

Title: US-10-027-725A-8  
Perfect score: 614  
Sequence: 1 LESGPGLVKPSQTLTLCTV.....RSDGYTLDNWGQGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	5	ABG30446 Human IGE
2	608	99.0	114	5	ABG30447 Human IGE
3	546	88.9	114	5	ABG30445 Human IGE
4	507	82.6	473	4	ABG36206 Human imm
5	504.5	82.2	117	7	ADC99784
6	504.5	82.2	117	7	ADC99784 Anti-huma
7	502.5	81.8	123	2	AAW78433
8	502.5	81.8	123	5	ABG97976
9	501	81.6	252	5	ABP45318
10	500.5	81.5	127	4	ABG80217
11	500	81.4	126	3	ABG30584
12	500	81.4	126	5	ABP54970
13	500	81.4	251	5	ABG80712
14	500	81.4	254	5	ABG80713
15	500	81.4	263	5	ABG80714
16	499.5	81.4	120	4	ABG2775
17	498	81.1	123	4	ABG2745
18	496.5	80.9	122	4	ABG2765
19	496	80.8	246	3	AAV15126
20	495	80.6	118	2	AAV06385
21	494.5	80.5	251	6	ABJ19829
22	494	80.5	172	3	AAV93713
23	494	80.5	172	6	AAE35892
24	493.5	80.4	117	7	ADC99776
25	493.5	80.4	117	7	ADD05380 Anti-MUC1

26	493.5	80.4	123	6	ADA89258	Human ant
27	493	80.3	120	6	ADA89198	Human ant
28	493	80.3	252	5	ABP45983	Human Bly
29	492.5	80.2	251	5	ABP44979	Human Bly
30	492.5	80.2	253	5	ABP45608	Human Bly
31	490.5	79.9	117	3	AAV44615	Human ant
32	490.5	79.9	580	6	AAO30915	di-NHS76
33	490.5	79.9	580	6	AAO30913	di-NHS76
34	488.5	79.6	119	2	AAW27554	Human Ab
35	488.5	79.6	119	6	ABJ18676	Antibody
36	488	79.5	118	2	AAV06383	Humanised
37	488	79.5	139	3	AAV56713	Amino aci
38	487.5	79.4	119	7	ADC99796	Anti-huma
39	487.5	79.4	119	7	ADD05400	Anti-MUC1
40	487	79.3	130	5	AAU81273	Human trk
41	487	79.3	254	5	ABP45567	Human Bly
42	487	79.3	256	5	ABP45596	Human Bly
43	484	78.8	117	4	AAU02540	Anti-adip
44	484	78.8	122	2	AAO30145	MAB 1-3-1
45	483.5	78.7	129	5	AAU81275	Human trk

## ALIGNMENTS

RESULT 1  
ABG30446  
ID ABG30446 standard; protein; 114 AA.  
XX AC ABG30446;  
XX DT 21-OCT-2002 (first entry)  
XX DE Human IGE Fab clone 60 heavy chain protein.  
XX KW Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;  
XX KM timothy grass pollen allergen; passive immunotherapy.  
XX OS Homo sapiens.  
XX FH Key  
XX FT Region Location/Qualifiers  
FT Region 1..26 /note= "FR1 region"  
FT Region 27..33 /note= "CDR1 region"  
FT Region 34..47 /note= "FR2 region"  
FT Region 48..63 /note= "CDR2 protein"  
FT Region 64..95 /note= "FR3 region"  
FT Region 96..103 /note= "CDR2 region"  
FT Region 104..114 /note= "FR4 region"  
XX WO200253595-A1.  
XX 11-JUL-2002.  
XX 27-DEC-2001; 2001WO-SE002908.  
XX 29-DEC-2000; 2000SE-00004892.  
(PAA ) PHARMACIA DIAGNOSTICS AB.  
XX Flicker S, Steinberger P, Kraft D, Valenta R;  
XX WPI; 2002-583604/62.  
XX N-PSDB; ABK89638.  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 37; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 60 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 100.0%; Score 614; DB 5; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-45;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLTLCTVSGGSIIRSGGYWVWVRQPPGKLEWIGNIYHSGNTYINPS 60  
 Db 1 LESGPGLVKPSQTLTLCTVSGGSIIRSGGYWVWVRQPPGKLEWIGNIYHSGNTYINPS 60  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114  
 Db 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 2

ABG30447  
 ID ABG30447 standard; protein; 114 AA.

XX AC ABG30447;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 100 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
Region	1..26
Region	/note= "FR1 region"
Region	27..33
Region	/note= "CDR1 region"
Region	34..47
Region	/note= "FR2 region"
Region	48..63
Region	/note= "CDR2 protein"
Region	64..95
Region	/note= "FR3 region"
Region	96..103
Region	/note= "CDR2 region"
Region	104..114
Region	/note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

PR 29-DEC-2000; 2000SE-00004992.

PA (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

DR N-PSDB; ABK9639.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 38; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for diagnosing a type  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 100 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 99.0%; Score 608; DB 5; Length 114;

Best Local Similarity 97.4%; Pred. No. 2.4e-44;

Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLTLCTVSGGSIIRSGGYWVWVRQPPGKLEWIGNIYHSGNTYINPS 60  
 Db 1 LESGPGLVKPSQTLTLCTVSGGSIIRSGGYWVWVRQPPGKLEWIGNIYHSGNTYINPS 60

QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114

Db 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 3

ABG30445

ID ABG30445 standard; protein; 114 AA.

XX AC ABG30445;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 94 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
Region	1..26
Region	/note= "FR1 region"
Region	27..33
Region	/note= "CDR1 region"
Region	34..47
Region	/note= "FR2 region"
Region	48..63
Region	/note= "CDR2 protein"
Region	64..95
Region	/note= "FR3 region"



FT	Region	96. .103	
FT	Region	/note= "CDR2 region"	
FT	Region	104. .114	
FT	Region	/note= "FR4 region"	
XX			
FN	WO200253595-A1.		
XX			
PD	11-JUL-2002.		
XX			
XX	27-DEC-2001; 2001WO-SE002908.		
PF			
XX	29-DEC-2000; 2000SE-00004892.		
PR			
XX	(PHAA ) PHARMACIA DIAGNOSTICS AB.		
PA			
XX	Flicker S, Steinberger P, Kraft D, Valenta R;		
PI			
XX	WPI; 2002-583604/62.		
DR	N-PSDB; ABK89637.		
XX			
XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising		
PT	variable region of group 2 allergen specific-human IgE Fabs, useful for		
PT	diagnosing or passive immunotherapy of type I allergy, for environmental		
PT	allergen detection.		
XX			
PS	Disclosure; Page 36; 45pp; English.		
XX			
CC	This invention relates to the DNA and protein sequences of group 2		
CC	allergen-specific human IgE Fabs and methods for their use. The proteins		
CC	of the invention may have antiallergic activities and may be used as a		
CC	vaccine or an inhibitor of binding of grass pollen allergen patient's IgE		
CC	antibodies to Phi p 2 (a major timothy grass pollen allergen). The group		
CC	2 allergen-specific Fabs of the invention may be useful for environmental		
CC	allergen detection and for standardisation of allergen extracts. The Fabs		
CC	- or a vaccine againsts a type I allergy is useful for passive		
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type		
CC	I allergy. The allergen-specific Fabs of the invention are useful for		
CC	inter alia, diagnosis, therapy and prevention of type I allergy. They are		
CC	also useful for identification of group 2 allergen-containing pollen and		
CC	may be used for blocking the binding of grass pollen allergic patients		
CC	IgE antibodies to Phi p 2. The present sequence represents the human IgG		
CC	Fab, clone 94 heavy chain protein of the invention		
XX			
SQ	Sequence 114 AA;		
<p>Query Match 88.9%; Score 546; DB 5; Length 114; Best Local Similarity 89.5%; Pred. No. 4.6e-39; Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;</p>			
QY	1	LESGPLVKPSQTLTLCTVSGGSIKGGYYSWVRQPPGKGLWIGNIYHSGNTYNP	60
Db	1	LESGPLVKPAQTLTLSCAVSGGSIKGGYYSWVRQPPGKGLWIGYIYHSGNTYNP	60
QY	61	LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS	114
Db	61	LKSRITMSVDTSENKFSRLNSVTAADTAVYVCARLDGYTLDIWGQGLTVTVSS	114
<p>RESULT 4 ID AAB36206 AC AAB36206; XX AAB36206; XX AAB36206; DT 15-FEB-2001 (first entry) XX Human immune system associated protein HISAP-4. XX Human; immune system associated protein; HISAP-4; immune disorder; KW infection; autoimmune disease; cancer. XX Homo sapiens. OS Homo sapiens. XX</p>			
FN	US6135941-A.		
XX			
PD	24-OCT-2000.		
XX			
PF	27-MAR-1998; 98US-00049672.		
XX			
PR	27-MAR-1998; 98US-00049672.		
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn KR;		
PI	Hillman JL, Au-Young J;		
XX			
DR	WPI; 2001-030926/04.		
DR	N-PSDB; AAC66522.		
XX			
PT	New human immune system associated proteins (HISAP) and polynucleotides		
PT	encoding the HISAP, useful for diagnosing, treating or preventing immune		
PT	or cell proliferative disorders or infections.		
XX			
PS	Claim 1; Col 53-56; 54pp; English.		
XX			
CC	The present invention provides the coding and protein sequences for a		
CC	number of human immune system associated proteins (HISAPs). These can be		
CC	used in the diagnosis and treatment of various autoimmune disorders,		
CC	infections and cell proliferation diseases. The diseases include AIDS,		
CC	adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,		
CC	Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia		
CC	gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus		
CC	erythematosus, arteriosclerosis, cirrhosis and cancer		
XX			
SQ	Sequence 473 AA;		
<p>Query Match 82.6%; Score 507; DB 4; Length 473; Best Local Similarity 79.8%; Pred. No. 4.3e-35; Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;</p>			
QY	2	ESGPGLVKPSQTLTLCTVSGGSIKGGYYSWVRQPPGKGLWIGNIYHSGNTYNP	61
Db	25	ESGPGLVKPSQTLTLCTVSGGSIKGGYYSWVRQPPGKGLWIGYIYHSGNTYNP	84
QY	62	KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSD-----GYTLDNWGQGLTVTVSS	114
Db	85	KSRITMSVDTSKNQFSLKLSVTAADTAVYVCARDVGLRGNGYGMVWGQGLTVTVSS	143
<p>RESULT 5 ID ADC99784 XX ADC99784 standard; protein; 117 AA. AC ADC99784; XX ADC99784; DT 01-JAN-2004 (first entry) XX Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13. XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast; XX lung cancer; human. OS Homo sapiens. XX WO2003057838-A2. XX WO2003057838-A2. PD 17-JUL-2003. XX 17-JUL-2003. PF 26-DEC-2002; 2002WO-US041581. XX 26-DEC-2002; 2002WO-US041581. PR 28-DEC-2001; 2001US-0346299P. XX 28-DEC-2001; 2001US-0346299P. PA (ABGE-) ABGENIX INC. XX (ABGE-) ABGENIX INC.</p>			

PI Gudas J;  
 XX WPI; 2003-587113/55.  
 DR N-PSDB; ADC95786.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease  
 PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX  
 XX Claim 1; SEQ ID NO 13; 78pp; English.  
 PS  
 XX The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumors, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumors, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 82.2%; Score 504.5; DB 7; Length 117;  
 Best Local Similarity 84.2%; Pred. No. 1.6e-35;  
 Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61  
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCAR-SDGYTLDNWQGLTVTVSS 114  
 DB 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYCAR-SDGYTLDNWQGLTVTVSS 117  
 RESULT 6  
 ADD05388  
 ID ADD05388 standard; protein; 117 AA.  
 AC ADD05388;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.  
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003057006-A2.  
 PN  
 XX 17-JUL-2003.  
 PD  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 PI Gudas J, Bar-Eli M;  
 XX WPI; 2003-577496/54.  
 DR N-PSDB; ADD05390.  
 XX  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX

PS Claim 1; SEQ ID NO 13; 87pp; English.  
 XX  
 CC The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the  
 CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 XX protein of the invention.  
 SQ Sequence 117 AA;  
 Query Match 82.2%; Score 504.5; DB 7; Length 117;  
 Best Local Similarity 84.2%; Pred. No. 1.6e-35;  
 Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 61  
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYINPSL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCAR-SDGYTLDNWQGLTVTVSS 114  
 DB 66 KSRVTISVDTSKNQFSLKSLSSVTAADTAVYCAR-SDGYTLDNWQGLTVTVSS 117  
 RESULT 7  
 AAW78433  
 ID AAW78433 standard; protein; 123 AA.  
 XX  
 AC AAW78433;  
 XX  
 DT 11-MAY-1999 (first entry)  
 DE Antibody heavy chain targeted to obr clone 26.  
 KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;  
 KW diagnosis; cancer; primer; PCR; amplification; diagnostic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9850431-A2.  
 PN  
 XX 12-NOV-1998.  
 PD  
 XX 30-APR-1998; 98WO-US008762.  
 PF  
 XX 02-MAY-1997; 97US-00850058.  
 PR  
 XX 24-JUN-1997; 97US-0050661P.  
 PD  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Arathoon R, Carter PJ, Merchant AM, Presta LG;  
 PI WPI; 1999-070091/06.  
 DR  
 XX Selective preparation of multispecific antibodies - with heteromultimeric  
 PT heavy chain and common light chain components, useful for, e.g. in vivo  
 PT diagnosis of cancer.  
 XX  
 XX Example 4; Fig 5; 69pp; English.  
 PS  
 XX This sequence represents the heavy chain variable region for an antibody  
 CC that binds to the obr clone 26 protein. The sequence encoding the chain  
 CC is generated by a new method for preparing a multispecific Ab comprising  
 CC a first polypeptide (pp) and at least 1 extra PP, where: (i) the first PP

comprises a multimerisation domain (MD) forming an interface positioned to interact with an interface of a MD of the extra PP; and (ii) the first and extra PPs each have a binding domain, which comprises a heavy chain and a light chain, where the variable light chains of the first and extra PPs comprise a common sequence. The method comprises: (a) culturing a host cell comprising nucleic acid encoding the first PP and extra PP, and the variable light chain, such that the nucleic acid is expressed; and (b) recovering the multispecific Ab from the culture. The method prepares heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins and Ab-immunoadhesin chimeras. The method allows for the enhanced formation of the desired heteromultimer relative to the undesired heteromultimers and homomultimers. The Abs can be used in immunoassays and for the in vitro or in vivo diagnosis of various diseases, such as cancer.

```

xx      Query Match          81.8%; Score 502.5; DB 2; Length 123;
SQ      Best Local Similarity 80.7%; Pred. No. 2.5e-35;
        Matches 96; Conservative 8; Mismatches 10; Indels 5; Gaps 1;

Qy      1  LESGPGHVKPSQTLSLACTTSGGSIRSGGYYSWVRPPGKGLDWIGNIYHSGMTYYNPS 60
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      5  VESGPGHLVKSPTLSLACTTSGGSISGGYYWSMIRCHPGKGLDWI GIIYYISGTTYNPS 64

Qy      61 LKSRITMSVTSKHFSLRLTSVTAADTAVTYCARS-----GYTLDNWGOGTILTVSS 114
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 LKRVTISVDTSKNQFSLKLSSTVAADTAVTYCARVLEIDYGSGASDYWGOGTILTVSS 123

```

```

RESULT 8
ABB97976
ID   ABB97976 standard; protein; 123 AA.
XX
XX   ABB97976;
XX   AC
XX   DT   06-SEP-2002 (first entry)

```

both polypeptides. Heteromultimers of the inventions include bispecific antibodies, bispecific immunoadhesins and antibody-immunoadhesin chimeras. The activity of antibodies of the invention may be described as, cytostatic, antibacterial and antiviral. The heteromultimer can be used for redirected cytotoxicity, for example to kill tumour cells, as a vaccine adjuvant, for delivering thrombolytic agents to clots, for converting enzyme activated prodrugs at a target site such as a tumour, for treating infectious diseases, for targeting immune complexes to cell surface receptors or for delivering immunotoxins to tumour cells. The current sequence represents the heavy chain variable region from antibody 123 AA; Sequence 123 AA;

```

SQ      Sequence 123 AA;
      Query Match      81.8%;      Score 502.5;      DB 5;      Length 123;
      Best Local Similarity 80.7%;      Pred. No. 2.5e-35;
      Matches 96;      Conservative 8;      Mismatches 10;      Indels 5;      Gaps 1

Qy      1  LESGPGHIVKPSQTLSLTCTVGSGSIRSGGGYVSWVRQPGKLEWIGNIYHSGNTYYNPS 60
      :      :      :      :      :      :      :      :      :      :      :
Db      5  VESGPGHIVKPSQTLSLTCTVGSGSISGGYVSWVRQPGKLEWIGNIYHSGNTYYNPS 64

Qy      61  LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSD-----GYTLDNWGQGLTVTVSS 114
      :      :      :      :      :      :      :      :      :      :      :
Db      65  LKSRVITSDVTSKQNFSLKLSVTAADTAVYICARVLDYCGSASDYWGQGLTVTVSS 123

```

RESULT 9  
ABP45318  
ID ABP45318 standard; protein; 352 AA.  
XX  
XX  
XX  
XX  
XX  
19-AUG-2002 (first entry)  
XX  
XX  
XX  
Human BlyS binding scFv SEQ ID 1329

PT New multispecific antibodies having heteromultimeric and common  
PT components are useful to direct treatment to a target site such  
PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant  
PT treat infectious disease.

PS Example 4; Fig 5; 36pp; English.

The invention relates to a new multispecific antibody, comprising at least two polypeptides (pp1 and pp2) which meet at a multiface, where pp1 has a multimerisation domain forming an interface positioned to interact with an interface of a multimerisation domain of pp2, and both polypeptides each comprise a binding domain consisting a heavy chain and a variable light chain, where the light chain has a sequence common to

CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX SQ Sequence 252 AA;

Query Match 81.6%; Score 501; DB 5; Length 252;  
 Best Local Similarity 78.5%; Pred. No. 7.1e-35;  
 Matches 95; Conservative 10; Mismatches 8; Indels 8; Gaps 2;

QY 2 ESGPLVKPSTLSLTCTVSGSIRSGGYWVQPPGKLEWIGNIYHSGNTYINPSL 61

DB 6 ESGPLVKPSTLSLTCTVSGSIRSGGYWVQPPGKLEWIGNIYHSGNTYINPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSD-----GYTL---DNWGQGTTLVTS 113

DB 66 KSRVTSVDTSKNHFSLRLTSVTAADTAVYVCARSDGYDILITGYPLHAFDINGKGLTVTS 125

QY 114 S 114

DB 126 S 126

RESULT 10

AAAG80217  
 ID AAG80217 standard; protein; 127 AA.

XX AC AAG80217;

XX DT 22-JAN-2002 (first entry)

XX DE Human autoantibody MICA-6 variable region light chain.

XX KW Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;  
 KW Glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;  
 KW polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;  
 KW variable region; light chain; MICA-6.

XX OS Homo sapiens.

XX PN EP1149914-A2.

XX PD 31-OCT-2001.

XX PR 29-MAR-2001; 2001EP-00107702.

XX PR 10-APR-2000; 2000DE-01017782.

XX PR 25-MAY-2000; 2000DE-01025840.

XX PA (LABO-) LAROR KOCH MERK GMBH.

XX PI Richter W, Rickert M, Rapp I, Dangel W;

XX DR WPI; 2001-640702/74.

XX DR N-PSDB; AA168766.

XX PT New fusion protein, useful for diagnosis of diabetes type I and other  
 PT metabolic diseases, is reactive with autoantibodies against both  
 PT glutamate decarboxylase and islet cell antigen.

XX PS Disclosure; Page 35-36; 68pp; German.

XX XX

CC This invention describes a novel fusion protein (I) that has, at its N-  
 CC terminus, one or more epitopes that bind specifically to autoantibodies  
 CC (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or  
 CC more epitopes that bind specifically to antibodies (Ab) directed against  
 CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding  
 CC it, vectors containing (II) and transformed cells, are useful for  
 CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,  
 CC polyglandular autoimmune syndrome or other autoimmune conditions  
 CC associated with AAb against GAD65 or IA2. (I) provides a rapid and simple  
 CC diagnosis of high specificity and sensitivity, capable of recognizing  
 CC antibodies against both IA2 and GAD65, simultaneously. Unlike known  
 CC fusions, where the GAD65 component is at the N-terminus, (I) contains  
 CC correctly folded conformational epitopes that can react with most MICA  
 CC autoantibodies. This sequence represents the human autoantibody MICA-6  
 CC variable region light chain used in the method of the invention

XX SQ Sequence 127 AA;

Query Match 81.5%; Score 500.5; DB 4; Length 127;  
 Best Local Similarity 78.0%; Pred. No. 3.8e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 9; Gaps 1;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVQPPGKLEWIGNIYHSGNTYINPS 60

DB 5 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVQPPGKLEWIGNIYHSGNTYINPS 64

QY 61 LKSRTMSVDTSKNHFSLRLTSVTAADTAVYVCARS-----DGYTLDNWGQGTTLVT 111

DB 65 LKSRTMSVDTSKNHFSLRLTSVTAADTAVYVCARSVTCYPDYGLDINGQGTTLVT 124

QY 112 VSS 114

DB 125 VSS 127

RESULT 11

AAAB30584  
 ID AAB30584 standard; protein; 126 AA.

XX AC AAB30584;

XX DT 19-MAR-2001 (first entry)

XX DE A human variable heavy chain region of anti-IgE antibody.

XX KW Anti-idiotype antibody; C-epsilon3 region; immunoglobulin E; IgE;  
 KW anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;  
 KW rhinitis; chronic urticaria; food allergy; IgE-mediated disease;  
 KW passive immunisation.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Region 30..37 /note= "complementarity determining region 1"

XX FT Region 51..67 /note= "complementarity determining region 2"

XX FT Region 100..115 /note= "complementarity determining region 3"

XX PN WO200063252-A1.

XX PD 26-OCT-2000.

XX PF 12-APR-2000; 2000WO-EF003288.

XX PR 14-APR-1999; 99GB-00008533.

XX PA (NOVS ) NOVARTIS AG.

XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX PI Kricek F, Stadler B, Vogel M;

XX XX



PA (MAUR/) MAURER P.  
PA (LECH/) LECHNER F.  
PA (ORTW/) ORTMANN R.  
PA (LUEO/) LUEOEND R.  
PA (STAU/) STAUFENBIEL M.  
PA (FREY/) FREY P.  
XX  
XX MAURER P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;  
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
XX  
XX MPI; 2002-636514/68.  
XX  
XX Molecular antigen array used in the production of vaccines for infectious  
PT diseases.  
XX  
XX Claim 38; Page 227; 418pp; English.  
XX  
XX The invention relates to a composition comprising: (a) a non-natural  
CC molecular scaffold comprising: (i) a core particle selected from: (1) a  
CC core particle of a non-natural origin; and (2) a core particle of natural  
CC origin; and (ii) an organiser comprising at least one first attachment  
CC site, where the organiser is connected to the core particle by at least  
CC one covalent bond; (b) an antigen or antigenic determinant with at least  
CC one second attachment site, where the antigen or antigenic determinant is  
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
CC attachment site is selected from: (i) an attachment site not naturally  
CC occurring with the antigen or antigenic determinant; and (ii) an  
CC attachment site naturally occurring with the antigen or antigenic  
CC determinant, where the second attachment site is capable of association  
CC through at least one non-peptide bond to the first attachment site; and  
CC where the antigen or antigenic determinant and the scaffold interact  
CC through the association to form an ordered and repetitive antigen array.  
CC Also included is a process for producing a non-naturally occurring  
CC ordered and repetitive antigen array. The composition is used in  
CC immunisation and as a vaccine for diseases such as influenza, graft  
CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
CC gravis, immunoproliferative disease lymphadenopathy,  
CC angioimmunoproliferative lymphadenopathy, Alzheimer's disease,  
CC osteoporosis and infectious diseases. The present sequence is a modified  
CC antigen for use in the array of the invention. The antigen is modified to  
CC possess a cleavage site (enterokinase or factor Xa) and a Cysteine-  
CC containing N- or C-terminal linker peptide which serves as the attachment  
CC point to a virus like particle or bacterial protein (the scaffold  
CC protein)  
XX  
XX SQ Sequence 251 AA;  
Query Match 81.4%; Score 500; DB 5; Length 251;  
Best Local Similarity 78.7%; Pred. No. 8.6e-35;  
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;  
QY 1 LBSGGLVPSOTLSITCTVSGSIRSGGYVSWVRQPPGKGLVIGTIVHSNTYVPS 60  
DB 20 LBSGGLVPSOTLSITCTVSGSIRSGGYVSWVRQPPGKGLVIGTIVHSNTYVPS 79  
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTV 112  
DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTV 139  
QY 113 SS 114  
DB 140 SS 141  
RESULT 14  
ABG80713  
ID ABG80713 standard; peptide; 254 AA.  
XX  
XX AC ABG80713;  
XX

XX  
DT  
XX  
DE  
XX  
KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;  
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mitein;  
KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
KW enterokinase; cysteine-containing linker.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200256907-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 21-JAN-2002; 2002WO-IB000168.  
XX  
XX 19-JAN-2001; 2001US-0262379P.  
XX 04-MAY-2001; 2001US-0288549P.  
XX 05-OCT-2001; 2001US-0326998P.  
XX 07-NOV-2001; 2001US-0331045P.  
XX  
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
XX (NOVS) NOVARTIS PHARMA AG.  
XX (MAUR/) MAURER P.  
XX (LECH/) LECHNER F.  
XX (ORTW/) ORTMANN R.  
XX (LUEO/) LUEOEND R.  
XX (STAU/) STAUFENBIEL M.  
XX (FREY/) FREY P.  
XX  
XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;  
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
XX  
XX MPI; 2002-636514/68.  
XX  
XX Molecular antigen array used in the production of vaccines for infectious  
PT diseases.  
XX  
XX Claim 38; Page 227; 418pp; English.  
XX  
XX The invention relates to a composition comprising: (a) a non-natural  
CC molecular scaffold comprising: (i) a core particle selected from: (1) a  
CC core particle of a non-natural origin; and (2) a core particle of natural  
CC origin; and (ii) an organiser comprising at least one first attachment  
CC site, where the organiser is connected to the core particle by at least  
CC one covalent bond; (b) an antigen or antigenic determinant with at least  
CC one second attachment site, where the antigen or antigenic determinant is  
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
CC attachment site is selected from: (i) an attachment site not naturally  
CC occurring with the antigen or antigenic determinant; and (ii) an  
CC attachment site naturally occurring with the antigen or antigenic  
CC determinant, where the second attachment site is capable of association  
CC through at least one non-peptide bond to the first attachment site; and  
CC where the antigen or antigenic determinant and the scaffold interact  
CC through the association to form an ordered and repetitive antigen array.  
CC Also included is a process for producing a non-naturally occurring  
CC ordered and repetitive antigen array. The composition is used in  
CC immunisation and as a vaccine for diseases such as influenza, graft  
CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
CC gravis, immunoproliferative disease lymphadenopathy,  
CC angioimmunoproliferative lymphadenopathy, Alzheimer's disease,  
CC osteoporosis and infectious diseases. The present sequence is a modified  
CC antigen for use in the array of the invention. The antigen is modified to  
CC possess a cleavage site (enterokinase or factor Xa) and a Cysteine-  
CC containing N- or C-terminal linker peptide which serves as the attachment  
CC point to a virus like particle or bacterial protein (the scaffold  
CC protein)  
XX  
XX SQ Sequence 251 AA;  
Query Match 81.4%; Score 500; DB 5; Length 251;  
Best Local Similarity 78.7%; Pred. No. 8.6e-35;  
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;  
QY 1 LBSGGLVPSOTLSITCTVSGSIRSGGYVSWVRQPPGKGLVIGTIVHSNTYVPS 60  
DB 20 LBSGGLVPSOTLSITCTVSGSIRSGGYVSWVRQPPGKGLVIGTIVHSNTYVPS 79  
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTV 112  
DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTV 139  
QY 113 SS 114  
DB 140 SS 141  
RESULT 14  
ABG80713  
ID ABG80713 standard; peptide; 254 AA.  
XX  
XX AC ABG80713;  
XX

CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is a modified  
 CC antigen for use in the array of the invention. The antigen is modified to  
 CC possess a cleavage site (enterokinase or factor Xa) and a Cysteine-  
 CC containing N- or C-terminal linker peptide which serves as the attachment  
 CC point to a virus like particle or bacterial protein (the scaffold  
 CC protein)  
 XX  
 XX Sequence 254 AA;  
 SQ  
 Query Match 81.4%; Score 500; DB 5; Length 254;  
 Best Local Similarity 78.7%; Pred. No. 8.8e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;  
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVNRQPGKLEWIGNIYHSGNTYNPFS 60  
 DB 20 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVNRQPGKLEWIGNIYHSGNTYNPFS 79  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARERGETGLYPYTYIDVWGGTGTTVV 112  
 DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARERGETGLYPYTYIDVWGGTGTTVV 139  
 QY 113 SS 114  
 DB 140 SS 141  
 RESULT 15  
 ABG80714  
 ID ABG80714 standard; protein; 263 AA.  
 AC ABG80714;  
 XX  
 XX 29-NOV-2002 (first entry)  
 DT  
 XX Human IgG/factor Xa cleavage site fusion protein from pCep--Xa-Fc\*.  
 DE  
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutan;  
 KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW immunoproliferative disease; myasthenia gravis; multiple sclerosis;  
 KW angioimmunoproliferative lymphadenopathy; Alzheimer's disease;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200256907-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 21-JAN-2002; 2002WO-IB000168.  
 XX  
 XX 19-JAN-2001; 2001US-0262379P.  
 PR 04-MAY-2001; 2001US-0288549P.  
 PR 05-OCT-2001; 2001US-0326998P.  
 PR 07-NOV-2001; 2001US-0331045P.  
 XX  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS ) NOVARTIS PHARMA AG.  
 PA (MAUR/) MAURER P.  
 PA (LECH/) LECHNER F.  
 PA (ORTM/) ORTMANN R.  
 PA (LUEO/) LUEOEND R.  
 PA (STAU/) STAUFENBIEL M.  
 PA (FREY/) FREY P.  
 XX

PI Maurer P, Lechner F, Ortman R, Lueoend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Seibel P, Piossek C;  
 XX WPI; 2002-636514/68.  
 DR N-PSDB; ABS66508.  
 XX  
 XX Molecular antigen array used in the production of vaccines for infectious  
 XX diseases.

Example 1; Fig 1; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural  
 XX molecular scaffold comprising: (i) a core particle selected from: (1) a  
 XX core particle of a non-natural origin; and (2) a core particle of natural  
 XX origin; and (ii) an organismer comprising at least one first attachment  
 XX site, where the organismer is connected to the core particle by at least  
 XX one covalent bond; (b) an antigen or antigenic determinant with at least  
 XX one second attachment site, where the antigen or antigenic determinant is  
 XX amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
 XX attachment site is selected from: (i) an attachment site not naturally  
 XX occurring with the antigen or antigenic determinant; and (ii) an  
 XX attachment site naturally occurring with the antigen or antigenic  
 XX determinant, where the second attachment site is capable of association  
 XX through at least one non-peptide bond to the first attachment site; and  
 XX where the antigen or antigenic determinant and the scaffold interact  
 XX through the association to form an ordered and repetitive antigen array.  
 XX Also included is a process for producing a non-naturally occurring  
 XX ordered and repetitive antigen array. The composition is used in  
 XX immunisation and as a vaccine for diseases such as influenza, graft  
 XX versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult  
 XX respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 XX acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 XX systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 XX gravis, immunoproliferative disease lymphadenopathy.  
 XX angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 XX rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 XX osteoporosis and infectious diseases. The present sequence is a modified  
 XX antigen for use in the array of the invention. The antigen is modified to  
 XX possess a cleavage site (enterokinase or factor Xa) and a Cysteine-  
 XX containing N- or C-terminal linker peptide which serves as the attachment  
 XX point to a virus like particle or bacterial protein (the scaffold  
 XX protein)

SQ Sequence 263 AA;

Query Match 81.4%; Score 500; DB 5; Length 263;  
 Best Local Similarity 78.7%; Pred. No. 9.1e-35;  
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVNRQPGKLEWIGNIYHSGNTYNPFS 60  
 DB 20 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVNRQPGKLEWIGNIYHSGNTYNPFS 79  
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSDG-----YTLDNWGGTGTTVV 112  
 DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARERGETGLYPYTYIDVWGGTGTTVV 139  
 QY 113 SS 114  
 DB 140 SS 141

Search completed: August 8, 2004, 12:13:46  
 Job time : 47.8091 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 38 5182 Seconds  
(without alignments)  
928.389 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLNMGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	14	US-10-027-725A-8
2	600	97.7	114	14	US-10-027-725A-9
3	546	88.9	114	14	US-10-027-725A-7
4	510.5	83.1	121	15	US-10-309-762-152
5	510	83.1	118	15	US-10-309-762-138
6	509.5	83.0	123	15	US-10-309-762-10
7	507.5	82.7	125	15	US-10-309-762-11
8	507	82.6	120	15	US-10-309-762-13
9	507	82.6	120	15	US-10-309-762-144
10	507	82.6	122	15	US-10-309-762-147
11	506	82.4	221	10	US-09-972-656-80
12	505.5	82.3	121	15	US-10-309-762-151
13	504.5	82.2	117	14	US-10-330-613-13
14	504.5	82.2	117	14	US-10-330-530-13
15	504.5	82.2	117	16	US-10-660-357-13

16	503.5	82.0	119	15	US-10-309-762-140
17	502.5	81.8	123	15	US-10-309-762-12
18	502	81.8	124	15	US-10-309-762-75
19	502	81.8	143	15	US-10-309-762-96
20	501	81.6	252	10	US-09-880-748-1329
21	501	81.6	252	12	US-10-293-418-1329
22	500	81.4	120	15	US-10-309-762-128
23	500	81.4	120	15	US-10-309-762-139
24	500	81.4	121	12	US-10-453-698-137
25	500	81.4	121	15	US-10-308-817-137
26	500	81.4	126	9	US-09-974-449-6
27	499.5	81.4	135	16	US-10-388-214A-34
28	499	81.3	116	15	US-10-309-762-127
29	498.5	81.2	125	15	US-10-309-762-8
30	498.5	81.2	125	15	US-10-309-762-16
31	497.5	81.0	119	15	US-10-309-762-131
32	497	80.9	110	15	US-10-309-762-74
33	496.5	80.9	123	15	US-10-309-762-9
34	496.5	80.9	127	15	US-10-309-762-14
35	495.5	80.7	113	15	US-10-309-762-148
36	495	80.6	118	14	US-10-078-757B-52
37	494.5	80.5	125	15	US-10-309-762-153
38	494.5	80.5	251	14	US-10-120-414-75
39	494	80.5	172	14	US-10-153-382-21
40	493.5	80.4	117	14	US-10-330-613-5
41	493.5	80.4	117	14	US-10-330-530-5
42	493.5	80.4	117	16	US-10-660-357-5
43	493.5	80.4	123	12	US-10-371-942-102
44	493.5	80.4	123	15	US-10-309-762-17
45	493	80.3	120	12	US-10-371-942-42

#### ALIGNMENTS

##### RESULT 1

US-10-027-725A-8  
; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; PRIOR APPLICATION DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-8

Query Match 100.0%; Score 614; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.5e-49;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LES	G	P	G	L	V	K	P	S	Q	T	L	S	T	C	T	V	S	G	S	I	R	S	G	G	Y	S	W	R	Q	P	G	K	G	L	E	W	I	G	N	T	Y	H	S	G	N	T	Y	N	P	S	60
Db	1	LES	G	P	G	L	V	K	P	S	Q	T	L	S	T	C	T	V	S	G	S	I	R	S	G	G	Y	S	W	R	Q	P	G	K	G	L	E	W	I	G	N	T	Y	H	S	G	N	T	Y	N	P	S	60
Qy	61	L	K	S	R	I	T	M	S	V	D	T	S	K	N	H	F	S	L	R	T	S	V	T	A	D	T	A	V	Y	C	A	R	S	D	G	T	L	N	W	G	G	T	L	T	V	S	114					
Db	61	L	K	S	R	I	T	M	S	V	D	T	S	K	N	H	F	S	L	R	T	S	V	T	A	D	T	A	V	Y	C	A	R	S	D	G	T	L	N	W	G	G	T	L	T	V	S	114					

##### RESULT 2

US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

```
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match      97.7%; Score 600; DB 14; Length 114;
Best Local Similarity 96.5%; Pred. No. 1.4e-47;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LESGGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPS 60
Db 1 LESGGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114
Db 61 LKSRVYMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      88.9%; Score 546; DB 14; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.3e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LESGGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPS 60
Db 1 LESGGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPS 60

Qy 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

```
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match      83.1%; Score 510.5; DB 15; Length 121;
Best Local Similarity 82.8%; Pred. No. 2.5e-39;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSD---GYTLDNWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVVYCAVYDILTGYAFDIWGQGLTVTVSS 121

RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      83.1%; Score 510; DB 15; Length 118;
Best Local Similarity 85.0%; Pred. No. 2.7e-39;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSRSGGYWVWVQPPGKGLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVVYCARYYGSGDYWGQGLTVTVSS 118

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

```
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      83.0%; Score 509.5; DB 15; Length 123;
Best Local Similarity 82.2%; Pred. No. 3.2e-39;
Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSGYLDYWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYYCARAGKYGGSYLDYWGQGLTVTVSS 123

RESULT 7
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-11

Query Match      82.7%; Score 507.5; DB 15; Length 125;
Best Local Similarity 81.7%; Pred. No. 4.9e-39;
Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSGYLDYWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYYCARTYVDFLTGYPDADFIWGQGLTVTVSS 125

RESULT 8
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      82.6%; Score 507; DB 15; Length 120;
Best Local Similarity 83.6%; Pred. No. 5.2e-39;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSGDYT---LDNMGGTGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYYCAR--DGINYWFDLWGRGLTVTVSS 120

RESULT 9
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      82.6%; Score 507; DB 15; Length 120;
Best Local Similarity 83.6%; Pred. No. 5.2e-39;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSVRQPPGKLEWIGNIYHSGNTYINPSSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSGDYT---LDNMGGTGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYYCAR--DGINYWFDLWGRGLTVTVSS 120

RESULT 10
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
```

```

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
;
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
;
; FILE REFERENCE: ABGENIX 027A
;
; CURRENT APPLICATION NUMBER: US/10/309,762
;
; CURRENT FILING DATE: 2002-12-02
;
; PRIOR APPLICATION NUMBER: 60/337275
;
; PRIOR FILING DATE: 2001-12-03
;
; NUMBER OF SEQ ID NOS: 246
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 147
;
; LENGTH: 122
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-10-309-762-147

```

	Query Match	82.6%	Score 507	DB 15	Length 122
	Best Local Similarity	82.1%	Pred. No. 5.3e-39		
	Matches 96	Conservative	8	Mismatches 9	Indels 4
					Gaps 1
QY	2	ESGPGIVKPSQTLSLTCTVSGSGSIRSGGYVMSVWRQPPGKLEWIGNIYHSGNTYYPNPSL	61		
Db	6	ESGPGIVKPSQTLSLTCTVSGSGSIRSGGYVMSVWRQPPGKLEWIGNIYHSGNTYYPNPSL	65		
QY	62	KSRITVSDVTSKNHFSRLRLTSVTAADTAVYYCAR---	SDGYTLDDNGQGTFLTVSS	114	
Db	66	KSRVITSDVTSKNQFSLKLSVTAADTAVYYCARYYDILT	CGYMDVWGQGTFLTVSS	122	

RESULT 11  
 US-09-972-656-80  
 ; Sequence 80, Application US/09972656  
 ; Publication No. US20030099647A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deshpande, Rajendra  
 ; APPLICANT: Tsai, Mei-Mei  
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
 ; TITLE OF INVENTION: Neutralizing Activity  
 ; FILE REFERENCE: A-799  
 ; CURRENT APPLICATION NUMBER: US/09/972, 656  
 ; CURRENT FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 80  
 ; LENGTH: 221  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-972-656-80

[illegible]

RESULT 12  
US-10-309-762-151  
; Sequence 151, Application US/10309762  
; Publication No. US2004001898A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Poltaz, Ian  
; APPLICANT: Hancu, Masahisa  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX  
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN  
; FILE REFERENCE: ARGENIX. 027A

```

; CURRENT APPLICATION NUMBER: US-10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151

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Query Match	82.3%	Score	505.5;	DB.15;	Length	121;
Best Local Similarity	82.8%	Pred.	No. 7.2e-39;			
Matches	96;	Conservative	8;	Mismatches	9;	Indels
					3;	Gaps
					1;	

  

Qy	2	ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMSVVRQPPGKGLEWIGNIYSGNTYTNPSL	61
Db	6	ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMSVVRQPPGKGLEWIGNIYSGNTYTNPSL	65
Qy	62	KSRITMSVDTSKNHFLSLRLTSVAADTAVYTCARS---	DGYTLDNWQGGTLVTYSS 114
Db	66	KSRVTSIDVTSKNQFSLKLSVVAADTAVYTCARVLLWFGYMDVWQGGTIVTVSS	121

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RESULT 13
US-10-330-613-13
; Sequence 13, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-330-613-13

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	Query Match	32.2%;	Score 504.5;	DB 14;	Length 117;
	Best Local Similarity	84.2;	Pred. No. 8.6e-39;		
	Matches 96;	Conservative	9;	Mismatches 6;	Indels 3; Gaps 2;
Qy	2	ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYIWSVWRQPPGKLEWIGNIYHSNGTYNPNSL	61		
Db	6	ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYIWTIRQPPGKLEWIGNIYHSNGTYNPNSL	65		
Qy	62	KSRITMSVDTSKNHFSURLTSVTAADTAVYYCAR-SDGYTLDNMGQQTLLTVSS	114		
Db	56	KSPVTIIVSDTSKNQFSKTSVTAADTAVYYCARFGDF--DYMGQGLTLTVSS	117		

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RESULT 14
US-10-330-530-13
; Sequence 13, Application US10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 13

```

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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-13

Query Match      82.2%; Score 504.5; DB 14; Length 117;
Best Local Similarity 84.2%; Pred. No. 8.6e-39;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

QY 2 ESGPLVKPSQTLSLTCTVSGGSIIRSGGYYSWVRQPGKGLEWIGNIYHSCNTYYNPSSL 61
Db 6 ESGPLVKPSQTLSLTCTVSGGSIIRSGGYYSWVRQPGKGLEWIGNIYHSCNTYYNPSSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREGDGF--DYWGQGLTVTVSS 117
```

```
RESULT 15
US-10-660-357-13
; Sequence 13, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: AGENTX:030CI
; CURRENT APPLICATION NUMBER: US/10/660,357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-13
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```
Query Match      82.2%; Score 504.5; DB 16; Length 117;
Best Local Similarity 84.2%; Pred. No. 8.6e-39;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

QY 2 ESGPLVKPSQTLSLTCTVSGGSIIRSGGYYSWVRQPGKGLEWIGNIYHSCNTYYNPSSL 61
Db 6 ESGPLVKPSQTLSLTCTVSGGSIIRSGGYYSWVRQPGKGLEWIGNIYHSCNTYYNPSSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREGDGF--DYWGQGLTVTVSS 117
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Search completed: August 8, 2004, 12:43:20  
Job time : 38.5182 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

QM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-8  
Perfect score: 614  
Sequence: 1 LBSGPGLVKPSQLSLTCTV.....RSDGYILDNWGQGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	82.6	473	3	US-09-049-672A-4
2	494	80.5	122	1	US-08-360-125-11
3	494	80.5	122	2	US-08-450-578-11
4	494	80.5	122	2	US-09-017-628-11
5	494	80.5	122	2	US-09-014-880-11
6	494	80.5	122	4	US-08-450-363-11
7	494	80.5	172	4	US-09-472-087-7
8	494	80.5	172	4	US-09-472-087-86
9	488.5	79.6	119	4	US-09-025-769B-39
10	488.5	79.6	119	4	US-09-025-769B-65
11	488	79.5	118	4	US-09-025-769B-25
12	478	77.9	487	4	US-09-800-729-145
13	473.5	77.1	119	5	US-08-360-125-5
14	473.5	77.1	119	2	US-08-450-578-5
15	473.5	77.1	119	2	US-09-017-628-5
16	473.5	77.1	119	2	US-09-014-880-5
17	473.5	77.1	119	4	US-08-450-363-5
18	459.5	74.8	142	2	US-08-480-774A-2
19	458.5	74.7	250	4	US-10-039-785-50
20	458	74.6	244	4	US-08-918-148-79
21	453	73.8	118	3	US-08-545-809A-116
22	453	73.8	126	1	US-08-276-852-142
23	453	73.8	126	1	US-08-899-575-142
24	453	73.8	126	1	US-08-899-575-142
25	453	73.8	126	5	PCT-US95-08743-142
26	446.5	72.7	119	2	US-08-652-816A-10
27	446	72.6	118	3	US-08-545-809A-123

Sequence 3, Appli  
Sequence 4, Appli  
Sequence 8, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 142, App  
Sequence 44, Appl  
Sequence 78, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 37, Appl  
Sequence 64, Appl  
Sequence 69, Appl

ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANTUT01

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/
; CLONE: 1513264
US-09-049-672A-4

Query Match      82.6%; Score 507; DB 3; Length 473;
Best Local Similarity 79.8%; Pred. No. 6.8e-43;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

QY      2  ESGFGLVKPSQTLSTCTVSGGSIIRSGGYWSVRQPPGKGLEWIGNTYHSGNTYINPFL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      25  ESGFGLVKPSETLSLTCAVSGGSIIRSGGYWSVRQPPGKGLEWIGYIYSGSTLYNPSL 84
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      62  KSRITMSVDTSKNHPSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGLTVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      85  KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARDDVGLRGNGYGMVWGQGLTVTVSS 143
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; OPERATING SYSTEM: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360.125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
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/
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match      80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.8e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY      2  ESGFGLVKPSQTLSTCTVSGGSIIRSGGYWSVRQPPGKGLEWIGNTYHSGNTYINPFL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  ESGFGLVKPSETLSLTCTVSGGSIIRSGGYWSVRQPPGKGLEWIGYIYSGSTLYNPSL 65
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      62  KSRITMSVDTSKNHPSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGLTVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARSGYGGYYGMVWGQGLTVTVSS 122
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-08-450-578-11
; Sequence 11, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450.578
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
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RESULT 4
US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match      80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.8e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1

QY      2  ESGPLVXPSOTLSLTCCTVSGGSIKSGGYVMSWVROPKGLGLEWIGNIYHSGNTYNNP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGPLVXPSFTLSLTCCTVSGGSISSSSYTWGVIKQPPKGLGLEWISGIIYSGSYTNNP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSD----GYTLDNWGGQTLVTWSS
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66  KSRVITISVDTSKNQFSLKLSVTAADTAVYVCARGSYGGYYGMDVWGQTLVTWSS
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994

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RESULT 7  
US-09-472-087-7  
; Sequence 7, Application US/09472087  
; Patent No. 668736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.



CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 79.6%; Score 488.5; DB 4; Length 119;  
Best Local Similarity 81.9%; Pred. No. 9.6e-42;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy 2 ESGGLVKPSQTLSTCTVSGGSTRGGYYSWVRQPPGKLEWIGNIYHSGNTYYPNPSL 61  
Db 6 ESGGLVKPSETLSLTCTVSGGSISS--YYMSWIRQPPGKLEWIGIYHSGNTYYPNPSL 63

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SPG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARWGGDGYFAMDYWGQGLTVTVSS 119

RESULT 11  
US-09-025-769B-25  
; Sequence 25, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-25

Query Match 79.5%; Score 488; DB 4; Length 118;  
Best Local Similarity 81.7%; Pred. No. 1.1e-41;  
Matches 94; Conservative 7; Mismatches 10; Indels 4; Gaps 2;

Qy 2 ESGGLVKPSQTLSTCTVSGGSTRGGYYSWVRQPPGKLEWIGNIYHSGNTYYPNPSL 61  
Db 6 ESGGLVKPSETLSLTCTVSGGSISS--YYMSWIRQPPGKLEWIGIYHSGNTYYPNPSL 63

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--RSDGYTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGGGVFDYWGQGLTVTVSS 118

RESULT 12  
US-09-800-729-145  
; Sequence 145, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 145  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-729-145

Query Match 77.9%; Score 478; DB 4; Length 487;  
Best Local Similarity 75.6%; Pred. No. 5.7e-40;  
Matches 93; Conservative 10; Mismatches 10; Indels 10; Gaps 2;

Qy 2 ESGGLVKPSQTLSTCTVSGGSTRGGYYSWVRQPPGKLEWIGNIYHSGNTYYPNPSL 61  
Db 25 ESGGLVKPSETLSLTCTVSGGSISSGGHYWSWIRQHPGKLEWIGIYSNGVTVYYPNPSL 84

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--DGYTL-----DNWGQGLTVT 111  
Db 85 KSRVTISVDTSKNQFSLRLSVTAADTAVYYCAKDRATRDGYLYRGGFYWGQGLTVT 144

Qy 112 VSS 114  
Db 145 VSS 147

RESULT 13  
US-08-360-125-5  
; Sequence 5, Application US/08360125  
; Patent No. 5767246

GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 57672461hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STANDARDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:

AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-5  
Query Match 77.1%; Score 473.5; DB 1; Length 119;  
Best Local Similarity 78.1%; Pred. No. 3e-40;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGYVWVROPKGLWIGNIYHSGNTYNP 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIRSGYVWVROPKGLWIGNIYHSGNTYNP 65  
QY 62 KSRITMSVTSKNHPSRLTSTVTAADTAVYICARSDGYT-LDNWGGTIVTVSS 114  
DB 66 KSRVTISLDTSKSQFSLKLSLTADTAVYICARSTRLRGADYWGQGTMTVTVSS 119  
RESULT 14  
US-08-450-578-5  
Sequence 5, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
RAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-5

Query Match 77.1%; Score 473.5; DB 2; Length 119;  
Best Local Similarity 78.1%; Pred. No. 3e-40;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
Qy 2 ESGPGLVKPSQTLTCTVSGGSTRGGYVWSVVRQPPGKGLEWIGNIYHSGNTYYNPSSL 61  
Db 6 ESGPGLVKPSQTLTCTVSGGSTRGGYVWSVVRQPPGKGLEWIGNIYHSGNTYYNPSSL 65  
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114  
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYYCARSTRIRGADYWGQGTMTVTVSS 119

RESULT 15

US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Toshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287ihiko  
APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-5

Query Match 77.1%; Score 473.5; DB 2; Length 119;  
Best Local Similarity 78.1%; Pred. No. 3e-40;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
Qy 2 ESGPGLVKPSQTLTCTVSGGSTRGGYVWSVVRQPPGKGLEWIGNIYHSGNTYYNPSSL 61  
Db 6 ESGPGLVKPSQTLTCTVSGGSTRGGYVWSVVRQPPGKGLEWIGNIYHSGNTYYNPSSL 65  
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114  
Db 66 KSRVTISLDTSKSQFSLKLSLTAADTAVYYCARSTRIRGADYWGQGTMTVTVSS 119

Search completed: August 8, 2004, 12:20:24  
Job time : 14.6455 secs



A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>

A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;

Best Local Similarity 82.8%; Pred. No. 6.1e-38; Mismatches 12; Indels 3; Gaps 1;

Matches 96; Conservative 5;

Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61

Db 32 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 91

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD---DGYTLDNWGQGTTLTVTSS 114

Db 92 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARPFLWFGEFLFDYWGQGTTLTVTSS 147

#### RESULT 3

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999

C;Accession: I37782; S25476

R;Demaion, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by h

A;Reference number: A36876; MUID:94113917; PMID:8290556

A;Accession: I37782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-128/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 80.2%; Score 492.5; DB 2; Length 140;

Matches 99; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61

Db 25 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 82

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD---GYTLDNWGQGTTLTVTSS 114

Db 83 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHNSSSWYGRYFDYWGQGTTLTVTSS 140

#### RESULT 4

S30534

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996

C;Accession: S30534

R;Mariette, X.

submitted to the EMBL Data Library, October 1992

A;Reference number: S30520

A;Accession: S30534

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-130 <MAR>

A;Cross-references: EMBL:Z19320

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 79.8%; Score 490; DB 2; Length 130;

Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61

Db 6 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGRIYTSGSTNYNPSSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----YT-----LDNWGQGTTL 109

Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDKGFWGSGYITRNSRAAFDIWGQGTM 125

Qy 110 VTSS 114

Db 126 VTSS 130

#### RESULT 5

S37456

Ig mu chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S37456

R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.

submitted to the EMBL Data Library, September 1993

A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from

A;Reference number: S37453

A;Accession: S37456

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-116 <MCI>

A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;6-90/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 79.6%; Score 488.5; DB 2; Length 116;

Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

Qy 6 GLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSLRSRV 65

Db 1 GLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSLRSRV 60

Qy 66 TMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-----LDNWGQGTTLTVSS 114

Db 61 TISVDTSKNQFSLKLSVTAADTAVYYCARG-GYSGYGYYVYMDVWGKGTTTVSS 116

#### RESULT 6

S31690

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31690

R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31690

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-130 <CUI>

A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;20-102/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 79.4%; Score 487.5; DB 2; Length 130;

Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61

Db 11 ESGPGLVKPSQTLTCTVSGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 68



C/Species: Homo sapiens (man)  
C/Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text change 16-Aug-1996

```
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;
Best Local Similarity 73.8%; Pred. No. 8.8e-36;
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 61
Db 25 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 84
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCAR-----SDGYTLDNWGGTLVTV 112
Db 85 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARVLVSRVTSISQSYIMDMVWGKTLVTV 144
Qy 113 SS 114
Db 145 SS 146

RESULT 12
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118,'E',120-121,'T',123-126,'F' <JON>
A;Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
Best Local Similarity 74.6%; Pred. No. 9.4e-36;
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 61
Db 6 QSGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARSDG-----YTLDNWGGTLVTV 112
Db 66 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARVTSWRSYLYKHYMDVMWGKTLVTV 125
Qy 113 SS 114
Db 126 SS 127

RESULT 13
```

```
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:g33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;
Best Local Similarity 78.4%; Pred. No. 9.4e-36;
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 61
Db 13 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 72
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCAR--SDGYTLDNWGGTLVTVSS 114
Db 73 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARIGNFGYGFDPWGGTLVTVSS 128

RESULT 14
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;
Best Local Similarity 82.6%; Pred. No. 1.1e-35;
Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 61
Db 25 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNSL 82
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARSDG--YTLDNWGGTLVTVSS 114
Db 83 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCARDAPLMYGMVDMVWGKTLVTVSS 137

RESULT 15
S26803
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26803
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
```

A:Accession: S26803  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-99 <WEN>  
 A:Cross-references: EMBL:Z14238; NID:G37710; PIDN:CAA78607.1; PID:G1335374  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>  
  
 Query Match 76.4%; Score 469; DB 2; Length 99;  
 Best Local Similarity 92.6%; Pred. No. 1.5e-35;  
 Matches 87; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 ESGGGLVKPSQTLTLCTVSGGSIRSGYXWIRPPGKLEWIGYIYHSGNTYINPSL 61  
 Db 6 ESGGGLVKPSQTLTLCTVSGGSIRSGYXWIRPPGKLEWIGYIYHSGNTYINPSL 65  
  
 QY 62 KSRVTMSVDTSKNHFSRLSSVTAADTAVYYCAR 95  
 Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99

Search completed: August 8, 2004, 12:18:54  
 Job time : 10.0182 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 6.21818 Seconds  
(without alignments)  
954.620 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LESGGLVKPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	439.5	71.6	129	1 HV2F HUMAN	P01824 homo sapien
2	420	68.4	146	1 HV2I HUMAN	P06331 mus musculus
3	393.5	64.1	117	1 HV2G HUMAN	P01825 homo sapien
4	372.5	60.7	137	1 HV46 MOUSE	P01822 mus musculus
5	357.5	58.2	113	1 HV47 MOUSE	P01823 mus musculus
6	349.5	56.9	144	1 HV43 MOUSE	P01819 mus musculus
7	348.5	56.8	116	1 HV61 MOUSE	P01832 mus musculus
8	347	56.5	117	1 HV62 MOUSE	P18533 mus musculus
9	342.5	55.8	116	1 HV60 MOUSE	P18531 mus musculus
10	330	53.7	135	1 HV02 XENLA	P20957 xenopus lae
11	313	51.0	120	1 HV2B HUMAN	P01815 homo sapien
12	302.5	49.3	119	1 HV2C HUMAN	P01816 homo sapien
13	293.5	47.8	136	1 HV01 XENLA	P20956 xenopus lae
14	291	47.4	122	1 HV3A HUMAN	P01762 homo sapien
15	289.5	47.1	125	1 HV2D HUMAN	P01817 homo sapien
16	289	47.1	114	1 HV3B HUMAN	P01763 homo sapien
17	288	46.9	115	1 HV44 MOUSE	P01820 mus musculus
18	288	46.8	147	1 HV2E HUMAN	P04438 homo sapien
19	287.5	46.8	121	1 HV2H HUMAN	P01818 homo sapien
20	287	46.7	119	1 HV40 MOUSE	P01810 mus musculus
21	286.5	46.7	117	1 HV2B RABIT	P01828 oryctolagus
22	282	45.9	122	1 HV3G HUMAN	P01768 homo sapien
23	280	45.6	126	1 HV2A HUMAN	P01814 homo sapien
24	278	45.3	116	1 HV05 CARAU	P19181 carassius a
25	277.5	45.2	121	1 HV3J HUMAN	P01771 homo sapien
26	277	45.1	119	1 HV37 MOUSE	P01807 mus musculus
27	276	45.0	116	1 HV45 MOUSE	P01821 mus musculus
28	276	45.0	136	1 HV2C RABIT	P01823 oryctolagus
29	274	44.8	119	1 HV38 MOUSE	P01808 mus musculus
30	274	44.6	114	1 HV2A RABIT	P01827 oryctolagus
31	272.5	44.4	117	1 HV41 MOUSE	P01811 mus musculus
32	272.5	44.4	117	1 HV42 MOUSE	P01812 mus musculus
33	272	44.3	122	1 HV3H_HUMAN	P01769 homo sapien

34	271.5	44.2	142	1 HV01 RAT	P01805 rattus norv
35	268	43.6	139	1 HV07 MOUSE	P01751 mus musculus
36	263.5	42.9	115	1 HV3D HUMAN	P01765 homo sapien
37	263	42.8	118	1 HV51 MOUSE	P06330 mus musculus
38	263	42.8	122	1 HV20 MOUSE	P01789 mus musculus
39	262.5	42.8	117	1 HV12 MOUSE	P01756 mus musculus
40	262	42.7	120	1 HV50 MOUSE	P06329 mus musculus
41	262	42.7	126	1 HV3K HUMAN	P01772 homo sapien
42	262	42.7	136	1 HV16 MOUSE	P01783 mus musculus
43	261.5	42.6	115	1 HV3F HUMAN	P01767 homo sapien
44	261.5	42.6	117	1 HV13 MOUSE	P01757 mus musculus
45	258.5	42.1	117	1 HV17 MOUSE	P01786 mus musculus

ALIGNMENTS

RESULT 1  
HV2F HUMAN  
ID HV2F HUMAN STANDARD; PRT; 129 AA.  
AC P01824;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region WAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestostomi;  
OC Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82222335; PubMed=6806818;  
RA Takahashi N., Teter D., Debuire B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02099; D2HUWA.  
DR HSSP; P01825; 7FAR.  
DR GlycosuiteDB; P01824; -.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 113 IG-LIKE.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.6%; Score 439.5; DB 1; Length 129;  
Best Local Similarity 66.7%; Pred. No. 6.4e-39;  
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;  
QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGYVSWIRQPPGKGLWIGYIYHSGNYNPSL 61  
Db 6 ESGPGLVKPSQTLSTCTVSGGSIKSGYVSWIRQPPGKGLWIGYIYHSGNYNPSL 65  
QY 62 KGRVTSVDTSKNHFSLRLSSVTAADTAVYCAR-----SDGYTLDNWGQGT 108  
Db 66 RGRVTSVDTSKNHFSLRLSSVTAADTAVYCAR-----SDGYTLDNWGQGT 123  
QY 109 LTVVSS 114  
Db 124 TVRVSS 129  
RESULT 2



RX MEDLINE=89238351; PubMed=2497341;  
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;  
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH  
RL gene segment.";  
RL Mol. Immunol. 26:431-434 (1989).  
RN [2]  
RX SEQUENCE OF 1-31.  
RP MEDLINE=78094475; PubMed=414225;  
RA Jilka R.L., Pectka S.;  
RT "Amino acid sequence of the precursor region of MOPC-315 mouse  
RL immunoglobulin heavy chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).  
RN [3]  
RX SEQUENCE OF 1-21.  
RP MEDLINE=79148758; PubMed=428562;  
RA Schechter I., Wolf O., Zemell R., Burstein Y.;  
RT "Structure and function of immunoglobulin genes and precursors.";  
RL Fed. Proc. 38:1839-1845 (1979).  
RN [4]  
RX SEQUENCE OF 19-136.  
RP MEDLINE=74170779; PubMed=4524622;  
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;  
RT "Amino acid sequence of the variable region of the heavy (alpha)  
RL chain of a mouse myeloma protein with anti-hapten activity.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).  
RN [5]  
RX REVISION TO 53.  
RP MEDLINE=77244979; PubMed=268248;  
RA Hood L., Margolies M.N., Givol D., Zakut R.;  
RL Unpublished results, cited by:  
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;  
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).  
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M27638; AAA61337.1; -;  
DR EMBL; X07860; CAA30727.1; -;  
DR PIR; PLO102; AVMS35.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.  
FT DOMAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 85 116 FRAMEWORK-3.  
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 127 137 FRAMEWORK-4.  
FT DISULFID 40 114 BY SIMILARITY.  
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).  
FT CONFLICT 15 15 G -> H (IN REF. 2).  
FT CONFLICT 77 78 GY -> YG (IN REF. 4).  
FT CONFLICT 102 102 N -> D (IN REF. 4).  
FT CONFLICT 123 123 MISSING (IN REF. 4).  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match

Best Local Similarity 60.7%; Score 372.5; DB 1; Length 137;

62.6%; Pred. No. 6.6e-32;

Matches 72; Conservative 18; Mismatches 22; Indels 3; Gaps 2;  
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWIRQPGKLEWIGYIYHSGNTYNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 24 ESGPGLVPSQTLSTCTVSGSIRSGGYWIRQPGKLEWIGYIYHSGNTYNPSL 82  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 83 KKRVSITRDTSENQFLKLSVTTEDTATYTCAGDNHDHLYYFDYWGQGLTVTVSS 137  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
RESULT 5  
HV47 MOUSE  
ID HV47 MOUSE STANDARD; PRT; 113 AA.  
AC P01823;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 36-60.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX STRAIN=A/J;  
RC MEDLINE=84024551; PubMed=6414509;  
RA Juszcak E.C., Margolies M.N.;  
RT "Amino acid sequence of the heavy chain variable region from the A/J  
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
RT idiotype.";  
RL Biochemistry 22:4291-4296 (1983).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE  
CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND  
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF  
CC STRAIN A/J MICE.  
CC PIR; A02098; G2MS60.  
DR PDB; 1J10; 18-FEB-03.  
DR PDB; 1J1P; 18-FEB-03.  
DR PDB; 1J1X; 18-FEB-03.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;  
Query Match 58.2%; Score 357.5; DB 1; Length 113;  
Best Local Similarity 62.8%; Pred. No. 1.9e-30;  
Matches 71; Conservative 16; Mismatches 21; Indels 5; Gaps 2;  
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWIRQPGKLEWIGYIYHSGNTYNPSL 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGGYWIRQPGKLEWIGYIYHSGNTYNPSL 63  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDGYTLDNWGQGLTVTVSS 114  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 64 KKRVSITRDTSENQFLKLSVTTEDTATYTCAGDNHDHLYYFDYWGQGLTVTVSS 113  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
RESULT 6  
HV43 MOUSE  
ID HV43 MOUSE STANDARD; PRT; 144 AA.  
AC P01819;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region MOPC 141 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Toneygawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 130 IG-LIKE.
FT NON TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 56.9%; Score 349.5; DB 1; Length 144;
Best Local Similarity 59.0%; Pred. No. 1.7e-29;
Matches 72; Conservative 18; Mismatches 21; Indels 11; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKGLWIGYVHSGNTYNP 61
DB 25 ESGPGLVAPQSLSLTCTVTGYSITS--GYSMHWIRQFPGNKLEWVGWIGNTSYNP 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCAR 112
DB 83 KSLRTITKNSQGVFLKMSLQTDOTARYCASVSYIYGRSDKYFTLDYWGQGTSTV 142
QY 113 SS 114
DB 143 SS 144

RESULT 7
HV61_MOUSE STANDARD; PRT; 116 AA.
ID HV61_MOUSE AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region I43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
DR PIR; JTO510; HVMS73.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 56.5%; Score 347; DB 1; Length 117;
Best Local Similarity 69.1%; Pred. No. 2.5e-29;
Matches 65; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

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DR PIR; JTO508; HVMS1B.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION I43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 56.8%; Score 348.5; DB 1; Length 116;
Best Local Similarity 71.3%; Pred. No. 1.7e-29;
Matches 67; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKGLWIGYVHSGNTYNP 61
DB 24 ESGPDLVKPSQSLTCTVTGYSITS--GYSMHWIRQFPGNKLEWVGWIGNTSYNP 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCAR 95
DB 83 KSRISITRDTSKNQFFLQLNSVTEDTAVYCAR 116

RESULT 8
HV62_MOUSE STANDARD; PRT; 117 AA.
ID HV62_MOUSE AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 733 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
DR PIR; JTO510; HVMS73.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 >117 IG-LIKE.
FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 56.5%; Score 347; DB 1; Length 117;
Best Local Similarity 69.1%; Pred. No. 2.5e-29;
Matches 65; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

```



QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGYVHSGNTYNNPSL 61  
Db 24 ESGPGLVKPSQSLTCTVGTGISTTGNYSWIRPPGKLEWIGYVHSGNTYNNPS 83  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR 95  
Db 84 KSRVTITRTDTSKNQFFLENNLSLTAEDTATYICAR 117

## RESULT 9

HV60\_MOUSE  
ID HV60\_MOUSE STANDARD; PRT; 116 AA.  
AC P18531;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region M15 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/cJ;  
RX MEDLINE=69279149; PubMed=2499654;  
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
the primary immune response";  
RL J. Exp. Med. 169:2007-2019 (1989).  
DR PIR; J0509; HVMS31.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig\_1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 18 IG HEAVY CHAIN V REGION M15.  
FT CHAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 54 67 FRAMEWORK-2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 85 116 FRAMEWORK-3.  
FT DISULFID 40 114 BY SIMILARITY.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 55.8%; Score 342.5; DB 1; Length 116;  
Best Local Similarity 68.1%; Pred. No. 7.3e-29;  
Matches 64; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGYVHSGNTYNNPSL 61  
Db 24 ESGPGLVKPSQSLTCTVGTGISTTGNYSWIRPPGKLEWIGYVHSGNTYNNPSL 82  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR 95  
Db 83 KNRISITRTDTSKNQFFLENNLSLTAEDTATYICAR 116

## RESULT 10

HV02\_XENLA  
ID HV02\_XENLA STANDARD; PRT; 135 AA.  
AC P20957;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region XIG14 precursor (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88176921; PubMed=2451244;  
RA Schwager J., Mikoryak C.A., Steiner L.A.;  
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced  
from cDNA sequence: implications for evolution of immunoglobulin  
domains";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; J03632; AAA49791.1; -.  
DR EMBL; J03632; AAA49791.1; -.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig\_1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 18  
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.  
FT DOMAIN 20 128 IG-LIKE.  
FT NON\_TER 135 135  
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;  
Query Match 53.7%; Score 330; DB 1; Length 135;  
Best Local Similarity 56.5%; Pred. No. 1.7e-27;  
Matches 65; Conservative 16; Mismatches 30; Indels 4; Gaps 2;  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKLEWIGYVHSGNTYNNPSL 61  
Db 23 ESGPGLVKPSQSLTCTVGTGISTTGNYSWIRPPGKLEWIGYVHSGNTADSL 80  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR--SDGYTLDNWGGTILVTSS 114  
Db 81 KNRVTITKNGKQVYQLQNGMEVKDTAMYICAREYASGYNFDYWGQGTMTVTTS 135  
RESULT 11  
HV2B\_HUMAN  
ID HV2B\_HUMAN STANDARD; PRT; 120 AA.  
AC P01815;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region COR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=70259837; PubMed=5449120;  
RA Press E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains";  
RL Biochem. J. 117:641-660 (1970).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02089; G1HUCO.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.

```

DR GO: 0003823; F: antigen binding; NAS.
DR GO: 0006955; P: immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110
FT MOD_RES 1 1
FT DISULFID 22 94
FT CARBOHYD 62 62
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

Query Match 51.0%; Score 313; DB 1; Length 120;
Best Local Similarity 56.3%; Pred. No. 9.1e-26;
Matches 67; Conservative 13; Mismatches 29; Indels 10; Gaps 3;

QY 2 ESGPGLVKPSQTLTCTVSGGSRGGYVSWIRQPPGKLEWIGYIYHSGNTYINPSSL 61
DB 6 ESGPALVKPTLTTLTCTFSFSSSTGMCVGNIRQPPGKLEWLARDWDDKYYNTSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDGYLDNWGGQGLVTVSS 114
DB 66 ETRLTISKDSRNQVLTMDPV---DTATYYCARITVTPAPAGY-MDVWGRGTPVTVSS 120

RESULT 12
HV2C HUMAN STANDARD; PRT; 119 AA.
ID HV2C_HUMAN
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; G1HUDV.
DR HSSP; P01789; 1MCP.
DR GO: 0005576; C: extracellular; NAS.
DR GO: 0003823; F: antigen binding; NAS.
DR GO: 0006955; P: immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113
FT MOD_RES 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 49.3%; Score 302.5; DB 1; Length 119;
Best Local Similarity 53.5%; Pred. No. 1.1e-24;
Matches 61; Conservative 17; Mismatches 35; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLTCTVSGGSRGGYVSWIRQPPGKLEWIGYIYHSGNTYINPSSL 61
DB 6 ESGPALVKPTLTTLTCTFSFSSSTGMCVGNIRQPPGKLEWLARDWDDKYYNTSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDGYLDNWGGQGLVTVSS 114
DB 66 ETRLTISKDSRNQVLTMDPV---DTATYYCARITVTPAPAGY-MDVWGRGTPVTVSS 120

RESULT 13
HV01 XENLA STANDARD; PRT; 136 AA.
ID HV01_XENLA
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG8 precursor (Fragment).
DE Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=98176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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or send an email to license@sib-sib.ch).
CC EMBL; M20484; AAA49774.1; ALT_TERM.
DR PIR; A31933; A31933.
DR HSSP; P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 136
FT DOMAIN 19 128
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match 47.8%; Score 293.5; DB 1; Length 136;
Best Local Similarity 52.1%; Pred. No. 1.1e-23;
Matches 61; Conservative 18; Mismatches 31; Indels 7; Gaps 3;

QY 2 ESGPGLVKPSQTLTCTVSGGSRGGYVSWIRQPPGKLEWIGYIYHSGNTYINPSSL 61
DB 23 ESGPGLVKPSQTLTCTVSGFELTS--YYVWIRQPPKLTLEWIGVVRTDGTADSL 80

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYC---ARSDGYLDNWGGQGLVTVSS 114
DB 81 KNRVTITKDGKQVYLQMNGMEVKDTAMYYCTSTAGTACY-FEHWGQGTMTVTVTS 136

RESULT 14
HV3A HUMAN STANDARD; PRT; 122 AA.
ID HV3A_HUMAN
AC P01762;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 31.2636 Seconds  
(without alignments)  
1150.508 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LESGFLVKPSQTLSTCTV.....RSDGYTLDNWGGQTLTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
1	480	78.2	478	Q72379	Q72379 homo sapien	
2	470.5	76.6	119	Q9UL73	Q9UL73 homo sapien	
3	469.5	76.5	492	Q72374	Q72374 homo sapien	
4	468	76.2	150	Q95973	Q95973 homo sapien	
5	460	74.9	496	Q96KX8	Q96KX8 homo sapien	
6	460	74.9	613	Q96EY0	Q96EY0 homo sapien	
7	441	71.8	139	Q868X2	Q868X2 homo sapien	
8	431	70.2	130	Q81ZD7	Q81ZD7 homo sapien	
9	429.5	70.0	588	Q8WUX4	Q8WUX4 homo sapien	
10	429.5	70.0	597	Q9BU10	Q9BU10 homo sapien	
11	429.5	70.0	618	Q96AA6	Q96AA6 homo sapien	
12	425.5	69.3	597	Q9BQ88	Q9BQ88 homo sapien	
13	412	67.1	473	Q8TC63	Q8TC63 homo sapien	
14	392.5	63.9	479	Q99M22	Q99M22 mus musculus	
15	389	63.4	116	Q723Y6	Q723Y6 homo sapien	
16	364	59.3	122	Q9UL75	Q9UL75 homo sapien	

17	344.5	56.1	121	4	Q9UL96	Q9UL96 homo sapien
18	343	55.9	118	11	Q811U5	Q811U5 mus musculus
19	340	55.4	121	11	Q99NG4	Q99NG4 mus musculus
20	336	54.7	482	11	Q91X92	Q91X92 mus musculus
21	314.5	51.2	118	4	Q9UL74	Q9UL74 homo sapien
22	298.5	48.6	493	4	Q8NCL6	Q8NCL6 homo sapien
23	295	48.0	484	11	Q8VEA0	Q8VEA0 mus musculus
24	295	48.0	613	4	Q8WUK1	Q8WUK1 homo sapien
25	294.5	48.0	116	4	Q9UL93	Q9UL93 homo sapien
26	291.5	47.5	113	4	Q9UL90	Q9UL90 homo sapien
27	291.5	47.5	597	4	Q96BB9	Q96BB9 homo sapien
28	290	47.2	118	4	Q9UL72	Q9UL72 homo sapien
29	288.5	47.0	481	11	Q91WT1	Q91WT1 mus musculus
30	287	46.7	147	4	Q9F509	Q9F509 homo sapien
31	285	46.4	118	4	Q9UL91	Q9UL91 homo sapien
32	284.5	46.3	119	5	Q9GYZ2	Q9GYZ2 schistosoma
33	283	46.1	145	11	Q924P7	Q924P7 mus musculus
34	283	46.1	145	11	Q924R1	Q924R1 mus musculus
35	282	45.9	145	11	Q924R4	Q924R4 mus musculus
36	280.5	45.7	121	4	Q9UL71	Q9UL71 homo sapien
37	280.5	45.7	486	11	Q91Z07	Q91Z07 mus musculus
38	280	45.6	469	11	Q8R3V9	Q8R3V9 mus musculus
39	277	45.1	124	6	Q9N0W6	Q9N0W6 oryctolagus
40	277	45.1	298	11	Q9QYF0	Q9QYF0 mus musculus
41	276.5	45.0	117	11	Q9QXE9	Q9QXE9 mus musculus
42	276	45.0	124	6	Q9N0W4	Q9N0W4 oryctolagus
43	276	45.0	143	11	Q924R0	Q924R0 mus musculus
44	275.5	44.9	499	4	Q8N5K4	Q8N5K4 homo sapien
45	275	44.8	494	4	Q96K68	Q96K68 homo sapien

ALIGNMENTS

RESULT 1  
Q72379  
ID Q72379 PRELIMINARY; PRT; 478 AA.  
AC Q72379;  
DT 01-OCT-2003 (Tremblrel. 25; Created)  
DT 01-OCT-2003 (Tremblrel. 25; Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25; Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN DKFZp686K04218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCS41F3217CA1 CRC64;

Query Match 78.2%; Score 480; DB 4; Length 478;  
Best Local Similarity 77.4%; Pred. No. 1.5e-41;  
Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;  
QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWGWIRQPPKGLGWIGYIVHSNTYNPSL 61  
Db 24 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWGWIRQPPKGLGWIGYIVHSNTYNPSL 83  
QY 62 KSRVTMSVDTSKNHSRLSSVTADTAITYYCARSQGY--TLDNWCQGLTVTVSS 114  
Db 84 ESRLSISIDTSKNQPSRLNLSLTAAADTAIFYFCARGVGLGTAFTDINGQGTVTWVSS 138  
RESULT 2  
Q9UL73

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ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match
Best Local Similarity 76.6%; Score 470.5; DB 4; Length 119;
Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 61
Db 6 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 63

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG---YTLNMGOGTLVTYSS 114
Db 64 KSRVTISVDRSKNQFSLRLTSLTAADTAVYCARLSNWNQPYFDYWGOGTLVTYSS 119

RESULT 3
Q7Z374 PRELIMINARY; PRT; 492 AA.
ID Q7Z374;
AC Q7Z374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN DKFZp686C02218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA Bloeker H., Boescher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -.
DE Hypothetical protein.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match
Best Local Similarity 76.5%; Score 469.5; DB 4; Length 492;
Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 61
Db 2 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 61

us-10-027-725a-9.rspt
Db 37 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 96
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCAR---SDGYTLDNMGOGTLVTYSS 114
Db 97 KSRLTIFVDTSKNHFSLRLTSLTAADTAVYCVRRHVEGPGYGW-FDPWGOGTLVTYSS 152

RESULT 4
O95973 PRELIMINARY; PRT; 150 AA.
ID O95973;
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 150
FT NON_TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match
Best Local Similarity 76.2%; Score 468; DB 4; Length 150;
Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 61
Db 25 ESGPGLVKPSTLSLCTCTVSGGSTRSGGYVSWIRQPPGKLEWIGYHSGNTYNPSSL 84

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDGYTLNMGOGTLVTYSS 114
Db 85 KSRVTISVDTSKNQFSLRLTSLTAADTAVYCARLGMGAFDFWGHGTMTYSS 137

RESULT 5
Q96KX8 PRELIMINARY; PRT; 496 AA.
ID Q96KX8;
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

```







OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle, and Lymph;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -.  
DR EMBL; BC001872; AAH01872.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 69.3%; Score 425.5; DB 4; Length 597;  
Best Local Similarity 72.5%; Pred. No. 9.6e-36;  
Matches 87; Conservative 6; Mismatches 16; Indels 11; Gaps 3;  
  
QY 4 GPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 63  
DB 27 GAGLLKPSLTCTCGVYGSP--SGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 84  
QY 64 RYVMSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG-YTLDNWGQGLTVTVSS 114  
DB 85 RVTISVDTSKKQLSLKSSVNAADTAVYYCARVITRASGTDGRYGMVWGQGLTVTVSS 144

RESULT 13  
Q8TC63 PRELIMINARY; PRT; 473 AA.  
AC Q8TC63;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Kidney;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC025985; AAH25985.1; -.  
DR GO; GO:005507; F-copper ion binding; IEA.  
DR GO; GO:0005489; F-electron transporter activity; IEA.  
DR GO; GO:0006118; P-electron transport; IEA.  
DR InterPro; IPR000923; BlueCu1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00196; COPPER\_BLUE; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 67.1%; Score 412; DB 4; Length 473;  
Best Local Similarity 69.0%; Pred. No. 1.8e-34;  
Matches 80; Conservative 11; Mismatches 19; Indels 6; Gaps 2;  
  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 61

Db 32 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 91  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTL-----DNWGQGLTVTVSS 113  
Db 92 RSRVTMSADMSSENFYKLDSVTAADTAVYYCAA--GHLVMFGFAHWGQGLVSVS 145

RESULT 14  
Q99M22 PRELIMINARY; PRT; 479 AA.  
AC Q99M22;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002091; AAH02091.1; -.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 63.9%; Score 392.5; DB 11; Length 479;  
Best Local Similarity 67.5%; Pred. No. 2e-32; Mismatches 16; Indels 3; Gaps 3;  
Matches 77; Conservative 16;  
  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 61  
Db 24 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPPGKLEWIGIYHSGNTYNNPSSL 82  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-LDNWGQGLTVTVSS 114  
Db 83 KNRSITRDTSKNQFLKLSVTTEDTATYYCA-SRGYSWFFNWGQGLTVTVSA 135

RESULT 15  
Q7Z3Y6 PRELIMINARY; PRT; 116 AA.  
AC Q7Z3Y6;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Rearranged VH4-34 V gene segment (Fragment).  
GN VH4-34.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hodgkin lymphoma;  
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,  
RA Hansmann M.L., Brauning A.;  
RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma  
RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg  
RT cell precursor in a germinal center."  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ564425; CAD92032.1; -.  
FT NON\_TER 1

FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12902 MW; CE3D8A84616C908 CRC64;  
Query Match 63.4%; Score 389; DB 4; Length 116;  
Best Local Similarity 68.5%; Pred. No. 7.9e-33;  
Matches 76; Conservative 9; Mismatches 14; Indels 12; Gaps 2;  
Qy 4 GPGLVKPSQTLSTCTVSGGSIKSGGYWIRQPPGKLEWIGYIYHSGNTYYPNPSLKS 63  
Db 8 GAGLLKPSSETLSLSCAVYGGSF--SGYYWNIWIRQPPGKLEWIGEIHNHSGSTYYPNPSLKS 65  
Qy 64 RVTMSVDTSKNHFSLRLSSVTADTAVYVCARSD-----GYTLDNW 104  
Db 66 RVTISVDTSKNQLSLKLSVTADTAVYVCARGEIVVVPAAASYYYMDVM 116

Search completed: August 8, 2004, 12:17:45  
Job time : 32.2636 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:00 ; Search time 46.8091 Seconds  
(without alignments)  
688.123 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LRSGPLVXPSQTSLTCTV.....RSDGYTLDNWGQGLTVVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1380s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	98.5	114	5	Abg30447 Human IGE
2	600	97.7	114	5	Abg30446 Human IGE
3	556	90.6	114	5	Abg30445 Human IGE
4	521	84.9	473	4	Aab36206 Human imm
5	516.5	84.1	123	2	Aaw78433 Antibody
6	516.5	84.1	123	5	Abb97976 Heavy cha
7	515.5	84.0	117	7	Adc99784 Anti-huma
8	515.5	84.0	117	7	Add05388 Anti-MUC1
9	513.5	83.6	120	4	Aab62775 Human HIV
10	512	83.4	123	4	Aab62745 Human HIV
11	510.5	83.1	122	4	Aab62765 Human HIV
12	510	83.1	246	3	Aay15126 Anti-muri
13	508	82.7	172	3	Aay93713 The heavy
14	508	82.7	172	6	Aae35892 Human 2.1
15	507.5	82.7	117	7	Adc99776 Anti-huma
16	507.5	82.7	117	7	Add05380 Anti-MUC1
17	507	82.6	126	3	AAB30384
18	507	82.6	126	5	ABP54970
19	507	82.6	251	5	ABG80712 Amyloid p
20	507	82.6	252	5	ABP45983
21	507	82.6	254	5	ABG80713 Amyloid p
22	507	82.6	263	5	ABG80714 Human IGG
23	506.5	82.5	251	6	Abj19829 Human VEG
24	506.5	82.5	253	5	ABP45608 Human Bly
25	503	81.9	252	5	ABP45318 Human Bly

## ALIGNMENTS

## RESULT 1

ABG30447  
ID ABG30447 standard; protein; 114 AA.

XX AC ABG30447;

XX AC

DT 21-OCT-2002 (first entry)

DE Human IgE Fab clone 100 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;

KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..26 /note= "FR1 region"

FT Region 27..33 /note= "CDR1 region"

FT Region 34..47 /note= "FR2 region"

FT Region 48..63 /note= "CDR2 protein"

FT Region 64..95 /note= "FR3 region"

FT Region 96..103 /note= "CDR2 region"

FT Region 104..114 /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX N-PSDB; ABK89639.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IGG comprising

XX variable region of group 2 allergen specific-human IGE Fabs, useful for

Aaw27554 Human Ab  
Abj18676 Antibody  
Aag80217 Human aut  
Aay06385 Humanised  
Aay56713 Amino aci  
Aau81273 Human trk  
Abp45596 Human Bly  
Adc99796 Anti-huma  
Add05400 Anti-MUC1  
Abb07171 ebvHGM M  
Ade28455 Human ant  
Ada89258 Human ant  
Aau81275 Human trk  
Ade28479 Human ant  
Aay06383 Humanised  
Adc99808 Anti-huma  
Add05412 Anti-MUC1  
Abp44979 Human Bly  
Ade28491 Human ant  
Ade28471 Human ant

26 502.5 81.8 119 2 AAW27554  
27 502.5 81.8 119 6 ABJ18676  
28 502.5 81.8 127 4 AAG80217  
29 502 81.8 118 2 AAY06385  
30 502 81.8 139 3 AAY56713  
31 501 81.6 130 5 AAU81273  
32 501 81.6 256 5 ABP45596  
33 497.5 81.0 119 7 ADC99796  
34 497.5 81.0 119 7 ADD05400  
35 496 80.8 121 5 ABB07171  
36 495.5 80.7 121 7 ADE28455  
37 495.5 80.7 123 6 ADA89258  
38 495.5 80.7 129 5 AAU81275  
39 495.5 80.7 466 7 ADE28479  
40 495 80.6 118 2 AAY06383  
41 494.5 80.5 121 7 ADC99808  
42 494.5 80.5 121 7 ADD05412  
43 494.5 80.5 251 5 ABP44979  
44 493.5 80.4 121 7 ADE28491  
45 493.5 80.4 466 7 ADE28471

PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 38; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 XX allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 100 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 98.5%; Score 605; DB 5; Length 114;  
 Best Local Similarity 99.1%; Pred. No. 2.6e-44;  
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIROPKGLWIGYIHSGNTYVPS 60

DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIROPKGLWIGYIHSGNTYVPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVVYCARSDGYTLDNWGQGLTVVSS 114

DB 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVVYCARSDGYTLDNWGQGLTVVSS 114

RESULT 2

ABG30446  
 ID ABG30446 standard; protein; 114 AA.

XX AC ABG30446;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 60 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 XX timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95
FT Region	/note= "FR3 region"
FT Region	96..103
FT Region	/note= "CDR2 region"
FT Region	104..114
FT Region	/note= "FR4 region"

PN WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX

29-DEC-2000; 2000SE-00004892.

(PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

DR N-PSDB; ABK89638.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.

XX Disclosure; Page 37; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC fab, clone 60 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 97.7%; Score 600; DB 5; Length 114;  
 Best Local Similarity 96.5%; Pred. No. 6.9e-44;  
 Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIROPKGLWIGYIHSGNTYVPS 60

DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIROPKGLWIGYIHSGNTYVPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVVYCARSDGYTLDNWGQGLTVVSS 114

DB 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVVYCARSDGYTLDNWGQGLTVVSS 114

RESULT 3

ABG30445  
 ID ABG30445 standard; protein; 114 AA.

XX AC ABG30445;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 94 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 XX timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95
FT Region	/note= "FR3 region"

FT Region 96. .103  
 FT /note= "CDR2 region"  
 FT Region 104. .114  
 FT /note= "FR4 region"  
 XX  
 PN WO200253595-A1.  
 XX  
 XX 11-JUL-2002.  
 XX  
 XX 27-DEC-2001; 2001WO-SE002908.  
 XX  
 XX 29-DEC-2000; 2000SE-00004892.  
 XX  
 XX (PHRA ) PHARMACIA DIAGNOSTICS AB.  
 XX  
 PI Flicker S, Steinberger P, Kraft D, Valenta R;  
 DR WPI; 2002-583604/62.  
 DR N-PSDB; ABK89637.  
 XX  
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX  
 PS Disclosure; Page 36; 45pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have anti-allergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to phi p 2. The present sequence represents the human IgG  
 CC fab, clone 94 heavy chain protein of the invention  
 XX  
 XX Sequence 114 AA;  
 SQ  
 Query Match 90.6%; Score 556; DB 5; Length 114;  
 Best Local Similarity 90.4%; Pred. No. 4e-40;  
 Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 LKSGPLVKPQTLSTCTVSGSIRSGGYWIRQPPKGLWIGTYIHSGNTYYPNS 60  
 Db 1 LKSGPLVKPQTLSTLSCAVSGSIRSGGYWIRQPPKGLWIGTYIHSGNTYYPNS 60  
 QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114  
 Db 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARLDGYTLIDWGGQGLTVTVSS 114  
 RESULT 4  
 ID AAB36206  
 XX AAB36206 standard; protein; 473 AA.  
 AC AAB36206;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human immune system associated protein HISAP-4.  
 XX  
 KW Human; immune system associated protein; HISAP-4; immune disorder;  
 KW infection; autoimmune disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX

PN US6135941-A.  
 XX  
 PD 24-OCT-2000.  
 XX  
 PF 27-MAR-1998; 98US-00049672.  
 XX  
 PR 27-MAR-1998; 98US-00049672.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
 PI Hillman JL, Au-Young J;  
 XX  
 XX WPI; 2001-030926/04.  
 DR N-PSDB; AAC66522.  
 XX  
 PT New human immune system associated proteins (HISAP) and polynucleotides  
 PT encoding the HISAP, useful for diagnosing, treating or preventing immune  
 PT or cell proliferative disorders or infections.  
 XX  
 PS Claim 1; Col 53-56; 54pp; English.  
 CC  
 CC The present invention provides the coding and protein sequences for a  
 CC number of human immune system associated proteins (HISAPs). These can be  
 CC used in the diagnosis and treatment of various autoimmune disorders,  
 CC infections and cell proliferation diseases. The diseases include AIDS,  
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
 CC erythematosus, arteriosclerosis, cirrhosis and cancer  
 XX  
 SQ Sequence 473 AA;  
 Query Match 84.9%; Score 521; DB 4; Length 473;  
 Best Local Similarity 83.2%; Pred. No. 1.7e-36;  
 Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;  
 QY 2 ESGPGLVKPQTLSTCTVSGSIRSGGYWIRQPPKGLWIGTYIHSGNTYYPNSL 61  
 Db 25 ESGPGLVKPQTLSTCTVSGSIRSGGYWIRQPPKGLWIGTYIHSGNTYYPNSL 84  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD-----GYTLDNWGQGLTVTVSS 114  
 Db 85 KSRVTISVDTSKNQFSLKSLSSVTAADTAVVYCARDDVGLRGNGYGMVWGQGLTVTVSS 143  
 RESULT 5  
 ID AAW78433  
 XX AAW78433 standard; protein; 123 AA.  
 AC AAW78433;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE Antibody heavy chain targeted to obr clone 26.  
 XX  
 KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;  
 KW diagnosis; cancer; primer; PCR; amplification; dicistronic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9850431-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 30-APR-1998; 98WO-US0008762.  
 XX  
 PR 02-MAY-1997; 97US-00850058.  
 PR 24-JUN-1997; 97US-0050661P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Arathoon R, Carter PJ, Merchant AM, Presta LG;

XX WPI; 1999-070091/06.  
 XX Selective preparation of multispecific antibodies - with heteromultimeric  
 PT heavy chain and common light chain components, useful for, e.g. in vivo  
 PT diagnosis of cancer.  
 XX  
 XX Example 4; Fig 5; 69pp; English.  
 XX  
 CC This sequence represents the heavy chain variable region for an antibody  
 CC that binds to the obr clone 26 protein. The sequence encoding the chain  
 CC is generated by a new method for preparing a multispecific Ab comprising  
 CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP  
 CC comprises a multimerisation domain (MD) forming an interface positioned  
 CC to interact with an interface of a MD of the extra PP; and (ii) the first  
 CC and extra PPs each have a binding domain, which comprises a heavy chain  
 CC and a light chain, where the variable light chains of the first and extra  
 CC PPs comprise a common sequence. The method comprises: (a) culturing a  
 CC host cell comprising nucleic acid encoding the first PP and extra PP, and  
 CC the variable light chain, such that the nucleic acid is expressed; and  
 CC (b) recovering the multispecific Ab from the culture. The method prepares  
 CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins  
 CC and Ab-immunoadhesin chimeras. The method allows for the enhanced  
 CC formation of the desired heteromultimer relative to the undesired  
 CC heteromultimers and homomultimers. The Abs can be used in immunoassays  
 CC and for the in vitro or in vivo diagnosis of various diseases, such as  
 CC cancer  
 XX  
 SQ Sequence 123 AA;

Query Match 84.1%; Score 516.5; DB 2; Length 123;  
 Best Local Similarity 84.0%; Pred. No. 1e-36;  
 Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;  
 QY 1 LESGPGLVKPSQTLSTCTVSGGSIRSGGYWWSWIRQPGKLEWIGYIYHSGNTYINPS 60  
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 5 VESGPGLVKPSQTLSTCTVSGGSIRSGGYWWSWIRQPGKLEWIGYIYHSGNTYINPS 64  
 QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD----GYTLDNWGQGLTVTVSS 114  
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 65 LKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARVDLEDYGGSGADYWGQGLTVTVSS 123

RESULT 6  
 ABB97976  
 ID ABB97976 standard; protein; 123 AA.  
 XX  
 AC ABB97976;  
 XX  
 DT 06-SEP-2002 (first entry)  
 XX  
 DE Heavy chain variable region from antibody obr.26.  
 XX  
 KW Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;  
 KW antiviral; vaccine; tumour.  
 XX  
 OS Synthetic.  
 XX  
 FN US2020262010-A1.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 23-MAY-2001; 2001US-00863693.  
 XX  
 PR 02-MAY-1997; 97US-0046816P.  
 PR 30-APR-1998; 98US-00070166.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Arathoon WR, Carter PU, Merchant AM, Presta LG;  
 XX  
 DR WPI; 2002-499676/53.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT New multispecific antibodies having heteromultimeric and common  
 PT components are useful to direct treatment to a target site such as a  
 PT tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to  
 PT treat infectious disease.  
 XX  
 XX Example 4; Fig 5; 36pp; English.

XX The invention relates to a new multispecific antibody, comprising at  
 CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1  
 CC has a multimerisation domain forming an interface positioned to interact  
 CC with an interface of a multimerisation domain of PP2, and both  
 CC polypeptides each comprise a binding domain consisting of a heavy chain and  
 CC a variable light chain, where the light chain has a sequence common to  
 CC both polypeptides. Heteromultimers of the inventions include bispecific  
 CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin  
 CC chimeras. The activity of antibodies of the invention may be described  
 CC as, cytostatic, antibacterial and antiviral. The heteromultimer can be  
 CC used for redirected cytotoxicity, for example to kill tumour cells, as a  
 CC vaccine adjuvant, for delivering thrombolytic agents to clots, for  
 CC converting enzyme activated prodrugs at a target site such as a tumour,  
 CC for treating infectious diseases, for targeting immune complexes to cell  
 CC surface receptors or for delivering immunotoxins to tumour cells. The  
 CC current sequence represents the heavy chain variable region from antibody  
 CC obr.26 used in the construction of bispecific antibodies  
 XX

SQ Sequence 123 AA;

Query Match 84.1%; Score 516.5; DB 5; Length 123;  
 Best Local Similarity 84.0%; Pred. No. 1e-36;  
 Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;  
 QY 1 LESGPGLVKPSQTLSTCTVSGGSIRSGGYWWSWIRQPGKLEWIGYIYHSGNTYINPS 60  
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 5 VESGPGLVKPSQTLSTCTVSGGSIRSGGYWWSWIRQPGKLEWIGYIYHSGNTYINPS 64  
 QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD----GYTLDNWGQGLTVTVSS 114  
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 65 LKSRVTISVDTSKNQFSLKLSVTAADTAVVYCARVDLEDYGGSGADYWGQGLTVTVSS 123

RESULT 7  
 ADC99784  
 ID ADC99784 standard; protein; 117 AA.  
 XX  
 AC ADC99784;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 13.  
 XX  
 KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;  
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;  
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;  
 KW lung cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003057838-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041581.  
 XX  
 PR 28-DEC-2001; 2001US-0346299P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas J;  
 XX  
 DR WPI; 2003-587113/55.  
 DR N-PSDB; ADC99786.  
 XX  
 PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.  
 PT tumors, cancers, and other malignancies.  
 XX Claim 1; SEQ ID NO 13; 78pp; English.  
 PS  
 XX The invention relates to a novel isolated monoclonal antibody comprising  
 CC a heavy or light chain amino acid or a heavy or light chain variable  
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the  
 CC invention demonstrates cytostatic activity and may be useful for treating  
 CC a disease or condition associated with the expression of MUC18 on the  
 CC cell surface such as tumours, specifically melanoma, oesophageal,  
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical  
 CC carcinomas and cervical intraepithelial neoplasia and cancers including  
 CC colorectal, breast or lung cancer, as well as other malignancies. The  
 CC current sequence is that of the anti-human MUC18 monoclonal antibody  
 CC heavy chain protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 84.0%; Score 515.5; DB 7; Length 117;  
 Best Local Similarity 86.8%; Pred. No. 1.2e-36;  
 Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNPSSL 61  
 Db 6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYSGSTYNPSSL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR-SDGYTLDNWGQGLTVTVSS 114  
 Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICAREGDF--DYWGQGLTVTVSS 117  
 RESULT 8  
 ADD05388  
 ID ADD05388 standard; protein; 117 AA.  
 AC  
 AC ADD05388;  
 XX  
 XX 01-JAN-2004 (first entry)  
 DT  
 DE Anti-MUC18 antibody heavy chain variable region protein, SEQ ID No 13.  
 XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;  
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003057006-A2.  
 PN  
 PD 17-JUL-2003.  
 XX  
 XX 26-DEC-2002; 2002WO-US041582.  
 PF  
 XX 28-DEC-2001; 2001US-0346460P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas J, Bar-Eli M;  
 PI  
 XX WPI; 2003-577496/54.  
 XX  
 DR N-PSDB; ADD05390.  
 DR  
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and  
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion  
 PT associated with melanoma, or increasing survival of an animal having a  
 PT metastatic tumor.  
 XX  
 XX Claim 1; SEQ ID NO 13; 87pp; English.  
 PS  
 XX The invention relates to a novel monoclonal antibody used for inhibiting  
 CC tumour growth in an animal. The tumour inhibition process comprises  
 CC selecting an animal in need of treatment for a tumour, providing a  
 CC monoclonal antibody comprising a heavy chain amino acid, where the

CC antibody consists of any one of 10 fully defined sequences of 117-123  
 CC amino acids given in the specification, and where the monoclonal antibody  
 CC binds MUC18, and contacting the tumour with the antibody resulting in  
 CC inhibited proliferation of the cells. The monoclonal antibody has  
 CC cytostatic and can be used in the production of a vaccine. The monoclonal  
 CC antibodies against the MUC18 antigen are useful for diagnosing and  
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or  
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or  
 CC increasing survival of an animal having a metastatic tumour. This  
 CC sequence represents an anti-MUC18 antibody heavy chain, variable region,  
 CC protein of the invention.  
 XX  
 SQ Sequence 117 AA;  
 Query Match 84.0%; Score 515.5; DB 7; Length 117;  
 Best Local Similarity 86.8%; Pred. No. 1.2e-36;  
 Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNPSSL 61  
 Db 6 ESGPGLVKPSQTLSLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYSGSTYNPSSL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR-SDGYTLDNWGQGLTVTVSS 114  
 Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICAREGDF--DYWGQGLTVTVSS 117  
 RESULT 9  
 AAB62775  
 ID AAB62775 standard; protein; 120 AA.  
 XX  
 AC AAB62775;  
 XX  
 XX 03-APR-2001 (first entry)  
 DT  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.  
 XX  
 XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200100678-A1.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-US017327.  
 PF  
 XX 30-JUN-1999; 99US-0141701P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Watkins BA, Reitz MS;  
 PI  
 XX WPI; 2001-112438/12.  
 DR  
 DR N-PSDB; AAF29076.  
 XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal.  
 XX  
 PS Claim 1; Page 69; 81pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection  
 XX  
 SQ Sequence 120 AA;  
 Query Match 83.6%; Score 513.5; DB 4; Length 120;  
 Best Local Similarity 86.2%; Pred. No. 1.8e-36;





PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-GE001350.  
 XX  
 PR 30-APR-1998; 98GB-00009280.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Lechler IR, Dörling A;  
 XX  
 DR WPI; 2000-038815/03.  
 DR N-PSDB; AAZ28998.  
 XX  
 XX Inhibiting T-cell mediated rejection of xenotransplanted organs.  
 PT  
 XX  
 PS Claim 9; Fig 11; 43pp; English.  
 XX  
 CC The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a  
 CC membrane-associated protein which binds to CTLA-4. Chimeric constructs  
 CC comprising DNA sequences encoding the extracellular domain of murine  
 CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.  
 CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated  
 CC T-cells and antagonises the co-stimulatory signal provided by the  
 CC interaction between donor B7 and recipient CD28. Cells expressing the  
 CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in  
 CC xenograft-specific immunosuppression  
 XX  
 XX Sequence 246 AA;  
 SQ  
 Query Match 83.1%; Score 510; DB 3; Length 246;  
 Best Local Similarity 85.0%; Pred. No. 7.6e-36;  
 Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
 QY 2 ESGPGLVKPSQILSLTCTVSGGSIRGGYVWSWIRPPGKLEWIGYIHSGNTYNPSL 61  
 DB 8 ESGPGLVKPSQILSLTCTVSGGSVSGSYVWSWIRPPGKLEWIGYIHSGNTYNPSL 67  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGGQTLTVSS 114  
 DB 68 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARMKDKFDYWGQGLTVTVSS 120  
 RESULT 13  
 AAY93713  
 ID AAY93713 standard; protein; 172 AA.  
 XX  
 AC AAY93713;  
 XX  
 DT 03-OCT-2000 (first entry)  
 XX  
 DE The heavy chain of immunoglobulin clone 2.1.1.3.  
 XX  
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
 KW proliferative disorder; cancer; immunodeficient disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200037504-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 23-DEC-1999; 99WO-US030895.  
 XX  
 PR 23-DEC-1998; 98US-0113647P.  
 XX  
 PA (PFIZ ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
 PI Corvalan JR;  
 XX  
 DR WPI; 2000-442647/38.

DR N-PSDB; AAA46876.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)  
 PT -4 containing specified heavy and light chain sequences, useful for  
 PT treating, e.g. immune disorders.  
 XX  
 PS Claim 2; Fig 1G; 157pp; English.  
 XX  
 CC The present sequence represents a heavy chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)  
 CC -4. Antibodies of the invention are composed of a heavy chain variable  
 CC region, comprising a modified contiguous sequence from a FR1-FR3 sequence  
 CC encoded by a human VH3-33 family gene. The modifications are contained in  
 CC CDR1, CDR2 and/or framework regions. The antibodies may be used to  
 CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity  
 CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and  
 CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be  
 CC used to up-regulate immune system to up-regulate immunodeficient  
 CC disorders  
 XX  
 SQ Sequence 172 AA;  
 Query Match 82.7%; Score 508; DB 3; Length 172;  
 Best Local Similarity 85.1%; Pred. No. 7.8e-36;  
 Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;  
 QY 3 SGPGLVKPSQILSLTCTVSGGSIRGGYVWSWIRPPGKLEWIGYIHSGNTYNPSLK 62  
 DB 1 SGPGLVKPSQILSLTCTVSGGSIRGGYVWSWIRPPGKLEWIGYIHSGNTYNPSLK 60  
 QY 63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDG--YTLDNWGGQTLTVSS 114  
 DB 61 SRVTISVDTSKNQFSLKLSVTAADTAVYVCARSDGYGIDVWGQGITTVTVSS 114  
 RESULT 14  
 AAE35892  
 ID AAE35892 standard; protein; 172 AA.  
 XX  
 AC AAE35892;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Human 2.1.1.3 anti-CTLA-4 antibody heavy chain.  
 XX  
 KW Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;  
 KW cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 24..31  
 FT /note= "Complementarity determining region (CDR) 1"  
 FT Region 45..61  
 FT /note= "Complementarity determining region (CDR) 2"  
 FT Region 94..103  
 FT /note= "Complementarity determining region (CDR) 3"  
 XX  
 PN EP1262193-A1.  
 XX  
 PD 04-DEC-2002.  
 XX  
 PF 23-MAY-2002; 2002EP-00253652.  
 XX  
 PR 23-MAY-2001; 2001US-0293042P.  
 XX  
 PA (PFIZ ) PFIZER PROD INC.  
 XX  
 PI Hanson DC, Mueller EE;  
 XX  
 DR WPI; 2003-131215/13.  
 XX  
 XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the

PT preparation of medicament for the treatment of cancer.

XX PS Disclosure; Fig 3; 76pp; English.

XX CC The invention relates to the use of human anti-cytotoxic T lymphocyte antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for the treatment of cancer such as bone cancer, pancreatic cancer, skin cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian cancer, cancer of the anal region, stomach cancer, breast cancer, testicular cancer, uterine cancer and carcinoma of the fallopian tubes. The present sequence is human anti-CTLA-4 antibody heavy chain

XX SQ Sequence 172 AA;

Query Match 82.7%; Score 508; DB 6; Length 172;

Best Local Similarity 85.1%; Pred. No. 7.8e-36;

Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 3 SGFGLVKPSQTLSTCTVSGGSIIRSGGYWWSWIRQPEKGLEWIGYIYHSGNTYYNPSLK 62

Db 1 SGFGLVKPSQTLSTCTVSGGSIIRSGGYWWSWIRQPEKGLEWIGYIYHSGNTYYNPSLK 60

Qy 63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGGQTLTVVSS 114

Db 61 SRVTISVDTSKNHFSLRLSSVTAADTAVYYCARSDGSDYIGIDVWGQGTITVTVSS 114

RESULT 15

ADC99776

ID ADC99776 standard; protein; 117 AA.

XX AC ADC99776;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody heavy chain protein SEQ ID 5.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytosstatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PT Gudas J;

XX WPI: 2003-587113/55.

XX N-PSDB; ADC99778.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

XX Claim 1; SEQ ID NO 5; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody heavy chain protein of the invention.

XX SQ Sequence 117 AA;

Query Match 82.7%; Score 507.5; DB 7; Length 117;

Best Local Similarity 86.8%; Pred. No. 5.8e-36;

Matches 99; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

Qy 2 ESGFGLVKPSQTLSTCTVSGGSIIRSGGYWWSWIRQPEKGLEWIGYIYHSGNTYYNPSL 61

Db 6 ESGFGLVKPSQTLSTCTVSGGSIIRSGGYWWSWIRQPEKGLEWIGYIYHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDGYTLDNWGGQTLTVVSS 114

Db 66 KSRVTISVDTSKNHFSLRLSSVTAADTAVYYCARGGDGXY--WGQGTITVTVSS 117

Search completed: August 8, 2004, 12:13:46

Job time : 46.8091 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:17:52 ; Search time 38.5182 Seconds  
(without alignments)  
928.389 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LESGPGLVKPSQTLSITCTV.....RSDGYTLDNWGGTILTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubpaa/PCT\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_PUB PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW PUB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	14	US-10-027-725A-9
2	600	97.7	114	14	US-10-027-725A-8
3	556	90.6	114	14	US-10-027-725A-7
4	524.5	85.4	121	15	US-10-309-762-152
5	524	85.3	118	15	US-10-309-762-138
6	523.5	85.3	123	15	US-10-309-762-118
7	521	84.9	120	15	US-10-309-762-113
8	521	84.9	120	15	US-10-309-762-144
9	521	84.9	122	15	US-10-309-762-147
10	520	84.7	221	15	US-09-972-656-80
11	519.5	84.6	121	15	US-10-309-762-151
12	519.5	84.6	125	15	US-10-309-762-11
13	517.5	84.3	119	15	US-10-309-762-140
14	516.5	84.1	123	15	US-10-309-762-12
15	516	84.0	124	15	US-10-309-762-75

16	516	84.0	143	15	US-10-309-762-96
17	515.5	84.0	117	14	US-10-330-613-13
18	515.5	84.0	117	14	US-10-330-530-13
19	515.5	84.0	117	16	US-10-660-357-13
20	514	83.7	120	15	US-10-309-762-128
21	514	83.7	120	15	US-10-309-762-139
22	514	83.7	121	12	US-10-453-698-137
23	514	83.7	121	15	US-10-308-817-137
24	513	83.6	116	15	US-10-309-762-127
25	512.5	83.5	125	15	US-10-309-762-8
26	512.5	83.5	125	15	US-10-309-762-16
27	511.5	83.3	119	15	US-10-309-762-131
28	511	83.2	110	15	US-10-309-762-74
29	510.5	83.1	123	15	US-10-309-762-9
30	510.5	83.1	127	15	US-10-309-762-14
31	508.5	82.8	125	15	US-10-309-762-153
32	508	82.7	172	14	US-10-153-382-21
33	507.5	82.7	117	14	US-10-330-613-5
34	507.5	82.7	117	14	US-10-330-530-5
35	507.5	82.7	117	16	US-10-660-357-5
36	507.5	82.7	123	15	US-10-309-762-17
37	507	82.6	126	9	US-09-974-449-6
38	507	82.6	252	10	US-09-880-748-1994
39	507	82.6	252	12	US-10-293-418-1994
40	506.5	82.5	119	15	US-10-309-762-143
41	506.5	82.5	251	14	US-10-120-414-75
42	506.5	82.5	253	10	US-09-880-748-1619
43	506.5	82.5	253	12	US-10-293-418-1619
44	505.5	82.3	123	15	US-10-309-762-18
45	505.5	82.3	123	15	US-10-309-762-19

#### ALIGNMENTS

#### RESULT 1

US-10-027-725A-9  
; Sequence 9, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:  
; APPLICANT: Flicker, Sabine  
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof  
; FILE REFERENCE: 25401-4  
; CURRENT APPLICATION NUMBER: US/10/027,725A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/259,436  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-725A-9

Query Match	100.0%	Score 614;	DB 14;	Length 114;
Best Local Similarity	100.0%	Pred. No. 1.6e-48;		
Matches 114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	LESGLVKVPSQTLSITCTVSGGIRSGGYVSWIRQPGKLEWIGYTHSGNTYVPS	60	
Db	1	LESGLVKVPSQTLSITCTVSGGIRSGGYVSWIRQPGKLEWIGYTHSGNTYVPS	60	
QY	61	LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDNWGGTILTVSS	114	
Db	61	LKSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGYTLDNWGGTILTVSS	114	

RESULT 2  
US-10-027-725A-8  
; Sequence 8, Application US/10027725A  
; Publication No. US20030082659A1  
; GENERAL INFORMATION:

```
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match      97.7%; Score 600; DB 14; Length 114;
Best Local Similarity 96.5%; Pred. No. 3e-47; Indels 0; Gaps 0;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      90.6%; Score 556; DB 14; Length 114;
Best Local Similarity 90.4%; Pred. No. 3.1e-43; Indels 0; Gaps 0;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGPGLVKPSQTLSTLCAVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRITMSVDTSENKFSRLNSVTAADTAVYICARLDGYTLIDIWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

```
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match      85.4%; Score 524.5; DB 15; Length 121;
Best Local Similarity 86.2%; Pred. No. 2.5e-40; Indels 3; Gaps 1;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSD--CYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARYDILTGAFDINGQGLTVTVSS 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      85.3%; Score 524; DB 15; Length 118;
Best Local Similarity 88.5%; Pred. No. 2.7e-40; Indels 0; Gaps 0;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIIRGGYWSWIRPPGKGLWIGYVHSGNTYINPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARYYGGSDYWGQGLTVTVSS 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
```

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; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      85.3%; Score 523.5; DB 15; Length 123;
Best Local Similarity 85.8%; Pred. No. 5.1e-40;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY  2  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 65
QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGVT---DGYTLDNWGGTTLVTSS 114
Db  66  KSRVTISVDTSKNQFSLKLSVTAADTAVYICARAGKYGGSYLDYWGQGLTTLVTSS 123

RESULT 7
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 5.1e-40;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY  2  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 65
QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGVT---LDNMGQGTTLVTSS 114
Db  66  KSRVTISVDTSKNQFSLKLSVTAADTAVYICAR-DGYNWYFDLWGRGTLVTSS 120

RESULT 8
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
```

```
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 5.1e-40;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY  2  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 65
QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDGVT---LDNMGQGTTLVTSS 114
Db  66  KSRVTISVDTSKNQFSLKLSVTAADTAVYICAR-DGYNWYFDLWGRGTLVTSS 120

RESULT 9
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match      84.9%; Score 521; DB 15; Length 122;
Best Local Similarity 85.5%; Pred. No. 5.2e-40;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY  2  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSQTLSTLCTVSGGSISSGGYWSWIRPPGKLEWIGYIYHSGNTYINPSL 65
QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR---SDGYTLDNWGGTTLVTSS 114
Db  66  KSRVTISVDTSKNQFSLKLSVTAADTAVYICARYDILTYGMDWVGQGTTLVTSS 122

RESULT 10
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099847A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
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; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; SEQ ID NO 11
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656--80

Query Match      84.7%; Score 520; DB 10; Length 221;
Best Local Similarity 86.7%; Pred. No. 1.2e-39;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY  2  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
Db   6  ESGPGLVKPSETLSLTCAVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSDGYFDYWGQGLTVTVSS 118

RESULT 11
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151

Query Match      84.6%; Score 519.5; DB 15; Length 121;
Best Local Similarity 86.2%; Pred. No. 7.1e-40;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY  2  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
Db   6  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARVLLWFGYMDVWGQGLTVTVSS 121

RESULT 12
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
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; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11

Query Match      84.6%; Score 519.5; DB 15; Length 125;
Best Local Similarity 83.3%; Pred. No. 7.3e-40;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;

QY  2  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
Db   6  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDNWGQGLTVTVSS 114
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARVYDFLTGYPDAFDIWGQGLTVTVSS 125

RESULT 13
US-10-309-762-140
; Sequence 140, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-140

Query Match      84.3%; Score 517.5; DB 15; Length 119;
Best Local Similarity 86.8%; Pred. No. 1.1e-39;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY  2  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
Db   6  ESGPGLVKPQTSLTCTVSGGSIIRSGGYWMSWIRQPPGKLEWIGYIYHSGNTYNNPSL 65

QY  62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-GYTLDNWGQGLTVTVSS 114
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGNYGMDVWGQGLTVTVSS 119

RESULT 14
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
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; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12

Query Match      84.1%; Score 516.5; DB 15; Length 123;
Best Local Similarity 83.9%; Pred.No. 1.4e-39;
Matches 99; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

QY  2  ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMIROPPGKGLEWIGYIYHSGNTYINPSL 61
Db   6  ESGPGLVKPSQTLSLTCTVSGGSISGGYWSWIRQHPGKGLEWIGYIYSGTTYINPSL 65
QY   62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR-----SDGYTLDNWQGGLTVTVSS 114
Db   66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARVLLWFGEDYGVVDWVGQGLTVTVSS 123

RESULT 15
US-10-309-762-75
; Sequence 75, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-75

Query Match      84.0%; Score 516; DB 15; Length 124;
Best Local Similarity 84.0%; Pred.No. 1.5e-39;
Matches 100; Conservative 6; Mismatches 7; Indels 6; Gaps 2;

QY  2  ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMIROPPGKGLEWIGYIYHSGNTYINPSL 61
Db   6  ESGPGLVKPSQTLSLTCTVSGGSISGGYWSWIRQHPGKGLEWIGYIYSGTTYINPSL 65
QY   62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSD-----GYT-LDNWQGGLTVTVSS 114
Db   66 KSRVTISVDTSKNQFSLKLSVTAADTAVYICARENVYDILTGFWFDPWGQGLTVTVSS 124

Search completed: August 8, 2004, 12:43:20
Job time : 38.5182 secs
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 8, 2004, 12:09:01 ; Search time 13.6455 Seconds  
(without alignments)  
431.306 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LESGFLVKPSQTLTLCTV.....RSDGYTLNMGQTLIVTSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	3	US-09-049-672A-4
2	508	82.7	172	4	US-09-472-087-7
3	508	82.7	172	4	US-09-472-087-86
4	502.5	81.8	119	4	US-09-025-769B-39
5	502.5	81.8	119	4	US-09-025-769B-65
6	496	80.8	122	1	US-08-360-125-11
7	496	80.8	122	2	US-08-450-578-11
8	496	80.8	122	2	US-09-017-628-11
9	496	80.8	122	2	US-09-014-880-11
10	496	80.8	122	4	US-08-450-363-11
11	492	80.1	487	4	US-09-800-729-145
12	491	80.0	118	4	US-09-025-769B-25
13	487.5	79.4	119	1	US-08-360-125-5
14	487.5	79.4	119	2	US-08-450-578-5
15	487.5	79.4	119	2	US-09-017-628-5
16	487.5	79.4	119	2	US-09-014-880-5
17	487.5	79.4	119	4	US-08-450-363-5
18	472	76.9	244	4	US-08-918-148-79
19	467	76.1	118	3	US-08-545-809A-116
20	466.5	76.0	142	2	US-08-480-774A-2
21	463.5	75.5	250	4	US-10-039-785-50
22	460.5	75.0	119	2	US-08-652-816A-10
23	460	74.9	278	3	US-09-260-527-3
24	457	74.4	118	3	US-08-545-809A-142
25	457	74.4	118	4	US-09-343-698-6
26	457	74.4	118	4	US-08-325-955-6
27	450.5	73.4	219	4	US-09-460-384-37

28 450 73.3 832 3 US-08-630-820-7 Sequence 7, Appli  
29 450 73.3 832 4 US-09-273-453-7 Sequence 7, Appli  
30 449 73.1 126 1 US-08-276-852-142 Sequence 142, App  
31 449 73.1 126 1 US-08-899-575-142 Sequence 142, App  
32 449 73.1 126 1 US-08-899-575-142 Sequence 142, App  
33 449 73.1 126 5 PCT-US95-08743-142 Sequence 123, App  
34 448 73.0 118 3 US-08-545-809A-123 Sequence 75, Appl  
35 446.5 72.7 98 1 US-08-478-039-75 Sequence 75, Appl  
36 446.5 72.7 98 1 US-08-478-039-75 Sequence 75, Appl  
37 446.5 72.7 123 1 US-08-137-117D-64 Sequence 64, Appl  
38 446.5 72.7 123 2 US-08-436-717-64 Sequence 64, Appl  
39 446.5 72.7 123 4 US-08-793-450-4 Sequence 64, Appl  
40 446.5 72.7 138 1 US-08-137-117D-69 Sequence 69, Appl  
41 446.5 72.7 138 2 US-08-436-717-69 Sequence 69, Appl  
42 446.5 72.7 472 4 US-08-793-450-8 Sequence 8, Appl  
43 444 72.3 150 4 US-09-582-337-14 Sequence 14, Appl  
44 442.5 72.1 124 1 US-08-478-039-78 Sequence 78, Appl  
45 442.5 72.1 124 1 US-08-476-349A-78 Sequence 78, Appl

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREMITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANCYTUT01

CLONE: 1513264  
US-09-049-672A-4  
Query Match 84.9%; Score 521; DB 3; Length 473;  
Best Local Similarity 83.2%; Pred. No. 1.6e-44;  
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61  
DB 25 ESGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 84  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114  
DB 85 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 143

RESULT 2  
US-09-472-087-7  
; Sequence 7, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-472-087-7  
Query Match 82.7%; Score 508; DB 4; Length 172;  
Best Local Similarity 85.1%; Pred. No. 9.9e-44;  
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3 SGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 62  
DB 1 SGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 60  
QY 63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114  
DB 61 SRVTISVDTSKNQFSLKLSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114

RESULT 3  
US-09-472-087-86  
; Sequence 86, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 85  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-86  
Query Match 82.7%; Score 508; DB 4; Length 172;  
Best Local Similarity 85.1%; Pred. No. 9.9e-44;  
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3 SGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 62  
DB 1 SGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 60  
QY 63 SRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114  
DB 61 SRVTISVDTSKNQFSLKLSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114

RESULT 4  
US-09-025-769B-39  
; Sequence 39, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

US-09-025-769B-39  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;  
Best Local Similarity 85.3%; Pred. No. 2.3e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPLVKPSQTLSTCTVSGGSRSGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61